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TECH CENTER 1600/2900

1

SEQUENCE LISTING

<110> Young, Robert

<120> Compounds for Targeting

<130> 43191-256808

<140> US 09/825,012

<141> 2001-04-03

<150> US 60/237,159

<151> 2000-10-02

<150> GB 0008049.9

<151> 2000-04-03

<160> 101

<170> PatentIn version 3.1

<210> 1

<211> 282

<212> PRT

<213> Homo sapiens

<400> 1

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20 25 30

Phe Gly Glu Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val
35 40 45

Gln Ile Leu Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp
 50 55 60

Ser His Leu Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp
 65 70 75 80

Ala Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn
 85 90 95

Ser Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser
 100 105 110

Ala Val Asp Ser Tyr Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn
 115 120 125

Asp Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe
 130 135 140

Thr Glu Val Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly
 145 150 155 160

Asp Ala Val Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val
 165 170 175

Gln Glu Lys Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn
 180 185 190

Ala Gly Cys Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu
 195 200 205

Trp Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr
 210 215 220

Thr Ala Thr Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly
 225 230 235 240

Met Leu Leu Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn
 245 250 255

Phe Gln Ala Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser
 260 265 270

Asp His Tyr Pro Val Glu Val Met Leu Lys

275

280

<210> 2

<211> 1039

<212> DNA

<213> Homo sapiens

<400> 2

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cattctcgtc atctctgagg acatcaccat catctcagga tgaggggcat gaagctgctg	180
ggggcgctgc tggcactggc ggccctactg cagggggccg tgtccctgaa gatcgcagcc	240
ttcaacatcc agacatttgg ggagaccaag atgtccaatg ccaccctcgt cagctacatt	300
gtgcagatcc tgagccgcta tgacatcgcc ctgggtccagg aggtcagaga cagccacctg	360
actgccgtgg ggaagctgct ggacaacctc aatcaggatg caccagacac ctatcactac	420
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cctgaccagg tgtctgcggt ggacagctac tactacgatg atggctgcga gccctgcggg	540
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agggagtttg ccattgttcc cctgcatgcg gccccggggg acgcagtagc cgagatcgac	660
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gttcccgact cggtctttcc ctttaacttc caggctgcct atggcctgag tgaccaactg	960
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<211> 260

<212> PRT

<213> Homo sapiens

<400> 3

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 20 25 30

Asp Ile Ala Leu Val Gln Glu Val Arg Asp Ser His Leu Thr Ala Val
 35 40 45

Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp Ala Pro Asp Thr Tyr His
 50 55 60

Tyr Val Val Ser Glu Pro Leu Gly Arg Asn Ser Tyr Lys Glu Arg Tyr
 65 70 75 80

Leu Phe Val Tyr Arg Pro Asp Gln Val Ser Ala Val Asp Ser Tyr Tyr
 85 90 95

Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn Asp Thr Phe Asn Arg Glu
 100 105 110

Pro Ala Ile Val Arg Phe Phe Ser Arg Phe Thr Glu Val Arg Glu Phe
 115 120 125

Ala Ile Val Pro Leu His Ala Ala Pro Gly Asp Ala Val Ala Glu Ile
 130 135 140

Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val Gln Glu Lys Trp Gly Leu
 145 150 155 160

Glu Asp Val Met Leu Met Gly Asp Phe Asn Ala Gly Cys Ser Tyr Val
 165 170 175

Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu Trp Thr Ser Pro Thr Phe
 180 185 190

Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr Thr Ala Thr Pro Thr His
 195 200 205

Cys Ala Tyr Asp Arg Ile Val Val Ala Gly Met Leu Leu Arg Gly Ala
 210 215 220

Val Val Pro Asp Ser Ala Leu Pro Phe Asn Phe Gln Ala Ala Tyr Gly
 225 230 235 240

Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp His Tyr Pro Val Glu
 245 250 255

Val Met Leu Lys
 260

<210> 4

<211> 783

<212> DNA

<213> Homo sapiens

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cggttcacag aggtcaggga gtttgccatt gttcccctgc atgcggcccc gggggacgca	420
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gaggacgtca tggtgatggg cgacttcaat gcgggctgca gctatgtgag accctcccag	540
tggtcatcca tccgcctgtg gacaagcccc accttccagt ggctgatccc cgacagcgct	600
gacaccacag ctacacccac gcactgtgcc tatgacagga tcgtgggttg agggatgctg	660
ctccgagggg ccgttggttc cgactcgggt cttcccttta acttccaggc tgcctatggc	720
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tga	783

<210> 5

<211> 161

<212> PRT

29
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<213> Homo sapiens

<400> 5

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Leu Gln Gly Ala Val Ser Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr
20 25 30

Phe Gly Glu Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val
35 40 45

Gln Ile Leu Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp
50 55 60

Ser His Leu Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp
65 70 75 80

Ala Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn
85 90 95

Ser Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser
100 105 110

Ala Val Asp Ser Tyr Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn
115 120 125

Asp Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe
130 135 140

Thr Glu Val Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly
145 150 155 160

Asp

<210> 6

<211> 858

<212> DNA

<213> Homo sapiens

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 atgtccaatg ccaccctcgt cagctacatt gtgcagatcc tgagccgcta cgacatcgcc 180
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 gtgagaccct ccagtggtc atccatccgc ctgtggacaa gcccacctt ccagtggctg 660
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 gttgcaggga tgctgctccg aggggccgtt gttcccgaact cggctcttcc ctttaacttc 780
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<210> 7

<211> 721

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG-1 light chain

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 atccagatga ccagagagccc aagcagcctg agcgccagcg tgggtgacag agtgaccatc 120
 acctgtaagt ccagtcagag ccttttatat agtagcaatc aaaagatcta cttggcctgg 180
 taccagcaga agccaggtaa ggctccaaag ctgctgatct actgggcatc cactagggaa 240
 tctgggtgtgc caagcagatt cagcggtagc ggtagcggta ccgacttcac cttcaccatc 300

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cggacgttcg gccaaaggac caaggtggaa atcaaacgaa ctgtggctgc accatctgtc 420
ttcatcttcc cgccatctga tgagcagttg aaatctggaa ctgcctctgt tgtgtgcctg 480
ctgaataact tctatcccag agaggccaaa gtacagtggg aggtggataa cgccctccaa 540
tcgggtaact cccaggagag tgtcacagag caggacagca aggacagcac ctacagcctc 600
agcagcaccc tgacgctgag caaagcagac tacgagaaac acaaagtcta cgctgcgaa 660
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<210> 8

<211> 730

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG-1 light chain

<400> 8

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gtgaccatca cctgtaagtc cagtcagagc cttttatata gtagcaatca aaagatctac 180
ttggcctggg accagcagaa gccaggtaag gctccaaagc tgctgatcta ctgggcatcc 240
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ttcaccatca gcagcctcca gccagaggac atcgccacct actactgcca gcaatattat 360
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gtgtgcctgc tgaataactt ctatcccaga gaggccaaag tacagtggaa ggtggataac 540
gccctccaat cgggtaactc ccaggagagt gtcacagagc aggacagcaa ggacagcacc 600
tacagcctca gcagcaccct gacgctgagc aaagcagact acgagaaaca caaagtctac 660
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gagtgttaga 730

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<210> 9

<211> 239

<212> PRT

<213> Artificial Sequence

<220>

<223> Humanised HMFG-1 light chain

<400> 9

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
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Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala
20 25 30

Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ser Ser Gln Ser Leu
35 40 45

Leu Tyr Ser Ser Asn Gln Lys Ile Tyr Leu Ala Trp Tyr Gln Gln Lys
50 55 60

Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu
65 70 75 80

Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
85 90 95

Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr
100 105 110

Cys Gln Gln Tyr Tyr Arg Tyr Pro Arg Thr Phe Gly Gln Gly Thr Lys
115 120 125

Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
130 135 140

Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
145 150 155 160

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
165 170 175

Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
 180 185 190

Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
 195 200 205

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
 210 215 220

Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 225 230 235

<210> 10

<211> 1404

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG-1 heavy chain

<400> 10

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tgcaaggctt ctggctacac cttcagtgcc tactggatag agtgggtgcg ccaggctcca	180
ggaaagggcc tcgagtgggt cggagagatt ttacctggaa gtaataattc tagatacaat	240
gagaagttca agggccgagt gacagtcact agagacacat ccacaaacac agcctacatg	300
gagctcagca gcctgaggtc tgaggacaca gccgtctatt actgtgcaag atcctacgac	360
tttgcctggg ttgcttactg gggccaaggg actctgggtca cagtctcctc agcctccacc	420
aaggggcccat cgggtcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg	480
gccctgggct gcctgggtcaa ggactacttc cccgaaccgg tgacgggtgtc gtggaactca	540
ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac	600
tcctcagca gcgtgggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc	660
aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt	720
gacaaaactc ¹⁷⁵ acacatgccc ¹⁷⁵ accgtgccc ¹⁷⁵ gcacctgaac tcctgggggg accgtcagtc	780
ttcctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca	840

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tgggagagca  atgggcagcc ggagaacaac tacaagacca cgcctcccg tctggactcc   1260
gacggctcct  tcttcctcta cagcaagctc accgtggaca agagcaggtg gcagcagggg   1320
aacgtcttct  catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc   1380
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<210> 11

<211> 15

<212> DNA

<213> Artificial Sequence

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<223> Hybrid hinge

<220>

<221> CDS

<222> (1)..(15)

<223>

<400> 11

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Asp Lys Thr His Thr
1          5

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15

<210> 12

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Hybrid hinge

<400> 12

Asp Lys Thr His Thr
1 5

<210> 13

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide linker

<400> 13

ccgggtaaag ggagcggcgg gctgaagatc gcagccttca ac

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<210> 14

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide linker

<400> 14

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42

<210> 15

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> Polypeptide linker

<400> 15

Leu	Ser	Leu	Ser	Pro	Gly	Lys	Gly	Ser	Gly	Gly	Leu	Lys	Ile	Ala	Ala
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Phe Asn

<210> 16

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide linker

<400> 16

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39

<210> 17

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide linker

<400> 17

gagagggaca gaggctttcc ctgcgcgccc gacttctag

39

<210> 18

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Polypeptide linker

<400> 18

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1				5					10					15	

Asn

<210> 19

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide linker

<400> 19

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36

<210> 20

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide linker

<400> 20

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<210> 21

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Polypeptide linker

<400> 21

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1				5					10					15	

<210> 22

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide linker

<400> 22

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<210> 23

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide linker

<400> 23

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<210> 24

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> Polypeptide linker

<400> 24

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Phe Asn

<210> 25

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide linker

<400> 25

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36

<210> 26

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide linker

<400> 26

ggtggcacgg gtcgtggact tccgcccgcac ttctag

36

<210> 27

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Polypeptide linker

<400> 27

Pro	Pro	Cys	Pro	Ala	Pro	Glu	Gly	Gly	Leu	Lys	Ile	Ala	Ala	Phe	Asn
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<210> 28

<211> 57

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide linker

<400> 28

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<210> 29

<211> 57

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide linker

<400> 29

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<210> 30

<211> 27

<212> PRT

<213> Artificial Sequence

<220>

<223> Polypeptide linker

<400> 30

Asp	Lys	Thr	His	Thr	Cys	Cys	Val	Glu	Cys	Pro	Pro	Cys	Pro	Ala	Pro
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Glu	Gly	Ser	Gly	Gly	Leu	Lys	Ile	Ala	Ala	Phe
			20					25		

<210> 31

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide linker

<400> 31

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<210> 32

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide linker

<400> 32

ctgttttgag tgtgtacgac acagctcaca ggtggcacag gtcgtggtct cccg 54

<210> 33

<211> 25

<212> PRT

<213> Artificial Sequence

<220>

<223> Polypeptide linker

<400> 33

Asp	Lys	Thr	His	Thr	Cys	Cys	Val	Glu	Cys	Pro	Pro	Cys	Pro	Ala	Pro
1				5					10					15	

Glu	Gly	Gly	Leu	Lys	Ile	Ala	Ala	Phe
			20					25

<210> 34

<211> 1554

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

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tgcaaggctt ctggctacac cttcagtgcc tactggatag agtgggtgcg ccaggctcca	180
ggaaagggcc tcgagtgggt cggagagatt ttacctggaa gtaataattc tagatacaat	240
gagaagttca agggccgagt gacagtcact agagacacat ccacaaacac agcctacatg	300
gagctcagca gcctgaggtc tgaggacaca gccgtctatt actgtgcaag atcctacgac	360
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gccctggggt gcctgggtcaa ggactacttc ccgaaccgg tgacgggtgtc gtggaactca	540
ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac	600
tcctcagca gcgtgggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc	660
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<210> 35

<211> 1554

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 35

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atgggatgga gctgtatcat cctcttcttg gtagcaacag ctacaggtgt ccactcccag 60
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tgcaaggctt ctggctacac cttcagtgcc tactggatag agtgggtgcg ccaggctcca 180
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gagctcagca gcctgaggtc tgaggacaca gccgtctatt actgtgcaag atcctacgac 360
tttgcttggg ttgcttactg gggccaaggg actctgggtc cagtctcctc agcctccacc 420
aagggcccat cgggtcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg 480

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tccctcagca gcgtgggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc 660
aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt 720
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<210> 36

<211> 1563

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 36

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aaggtgtcct gcaaggcttc tggctacacc ttcagtgcct actggataga gtgggtgcgc 180

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gcctacatgg agctcagcag cctgaggtct gaggacacag ccgtctatta ctgtgcaaga	360
tcctacgact ttgcctgggt tgcttactgg ggccaaggga ctctgggtcac agtctcctca	420
gcctccacca agggcccatc ggtcttcccc ctggcacccct cctccaagag cacctctggg	480
ggcacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggt gacgggtgtcg	540
tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca	600
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gacaccacag ctacaccac gcactgtgcc tatgacagga tcgtgggtgc agggatgctg	1440
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<210> 37

<211> 1554

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<220>

<221> CDS

<222> (1)..(1554)

<223>

<400> 37

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Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly	
1 5 10 15	
gtc cac tcc cag gtg cag ctg gtg cag tct ggg gca gag gtg aaa aag	96
Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys	
20 25 30	
cct ggg gcc tca gtg aag gtg tcc tgc aag gct tct ggc tac acc ttc	144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe	
35 40 45	
agt gcc tac tgg ata gag tgg gtg cgc cag gct cca gga aag ggc ctc	192
Ser Ala Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu	
50 55 60	
gag tgg gtc gga gag att tta cct gga agt aat aat tct aga tac aat	240
Glu Trp Val Gly Glu Ile Leu Pro Gly Ser Asn Asn Ser Arg Tyr Asn	
65 70 75 80	
gag aag ttc aag ggc cga gtg aca gtc act aga gac aca tcc aca aac	288
Glu Lys Phe Lys Gly Arg Val Thr Val Thr Arg Asp Thr Ser Thr Asn	
85 90 95	
aca gcc tac atg gag ctc agc agc ctg agg tct gag gac aca gcc gtc	336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val	
100 105 110	
tat tac tgt gca aga tcc tac gac ttt gcc tgg ttt gct tac tgg ggc	384
Tyr Tyr Cys Ala Arg Ser Tyr Asp Phe Ala Trp Phe Ala Tyr Trp Gly	
115 120 125	
caa ggg act ctg gtc aca gtc tcc tca gcc tcc acc aag ggc cca tcg	432
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser	
130 135 140	
gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg	480
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala	
145 150 155 160	
gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg	528
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val	
165 170 175	

tcg	tgg	aac	tca	ggc	gcc	ctg	acc	agc	ggc	gtg	cac	acc	ttc	ccg	gct	576
Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	
			180					185					190			
gtc	cta	cag	tcc	tca	gga	ctc	tac	tcc	ctc	agc	agc	gtg	gtg	acc	gtg	624
Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	
		195					200					205				
ccc	tcc	agc	agc	ttg	ggc	acc	cag	acc	tac	atc	tgc	aac	gtg	aat	cac	672
Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	
	210					215					220					
aag	ccc	agc	aac	acc	aag	gtg	gac	aag	aaa	gtt	gag	ccc	aaa	tct	tgt	720
Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	
225					230					235					240	
gac	aaa	act	cac	aca	tgc	cca	ccg	tgc	cca	gca	cct	gaa	ggg	agc	ggc	768
Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Gly	Ser	Gly	
				245					250					255		
ggg	ctg	aag	atc	gca	gcc	ttc	aac	atc	cag	aca	ttt	ggg	gag	acc	aag	816
Gly	Leu	Lys	Ile	Ala	Ala	Phe	Asn	Ile	Gln	Thr	Phe	Gly	Glu	Thr	Lys	
			260				265						270			
atg	tcc	aat	gcc	acc	ctc	gtc	agc	tac	att	gtg	cag	atc	ctg	agc	cgc	864
Met	Ser	Asn	Ala	Thr	Leu	Val	Ser	Tyr	Ile	Val	Gln	Ile	Leu	Ser	Arg	
		275					280					285				
tac	gac	atc	gcc	ctg	gtc	cag	gag	gtc	aga	gac	agc	cac	ctg	act	gcc	912
Tyr	Asp	Ile	Ala	Leu	Val	Gln	Glu	Val	Arg	Asp	Ser	His	Leu	Thr	Ala	
	290					295					300					
gtg	ggg	aag	ctg	ctg	gac	aac	ctc	aat	cag	gac	gca	cca	gac	acc	tat	960
Val	Gly	Lys	Leu	Leu	Asp	Asn	Leu	Asn	Gln	Asp	Ala	Pro	Asp	Thr	Tyr	
305					310					315					320	
cac	tac	gtg	gtc	agt	gag	cca	ctg	gga	cgg	aac	agc	tat	aag	gag	cgc	1008
His	Tyr	Val	Val	Ser	Glu	Pro	Leu	Gly	Arg	Asn	Ser	Tyr	Lys	Glu	Arg	
				325					330					335		
tac	ctg	ttc	gtg	tac	agg	cct	gac	cag	gtg	tct	gcg	gtg	gac	agc	tac	1056
Tyr	Leu	Phe	Val	Tyr	Arg	Pro	Asp	Gln	Val	Ser	Ala	Val	Asp	Ser	Tyr	
			340					345					350			
tac	tac	gat	gat	ggc	tgc	gag	ccc	tgc	ggg	aac	gac	acc	ttc	aac	cga	1104
Tyr	Tyr	Asp	Asp	Gly	Cys	Glu	Pro	Cys	Gly	Asn	Asp	Thr	Phe	Asn	Arg	
		355					360					365				
gag	cca	gcc	att	gtc	agg	ttc	ttc	tcc	cgg	ttc	aca	gag	gtc	agg	gag	1152
Glu	Pro	Ala	Ile	Val	Arg	Phe	Phe	Ser	Arg	Phe	Thr	Glu	Val	Arg	Glu	
	370					375					380					
ttt	gcc	att	gtt	ccc	ctg	cat	gcg	gcc	ccg	ggg	gac	gca	gta	gcc	gag	1200
Phe	Ala	Ile	Val	Pro	Leu	His	Ala	Ala	Pro	Gly	Asp	Ala	Val	Ala	Glu	
385					390					395					400	
atc	gac	gct	ctc	tat	gac	gtc	tac	ctg	gat	gtc	caa	gag	aaa	tgg	ggc	1248
Ile	Asp	Ala	Leu	Tyr	Asp	Val	Tyr	Leu	Asp	Val	Gln	Glu	Lys	Trp	Gly	
				405					410					415		

ttg gag gac gtc atg ttg atg ggc gac ttc aat gcg ggc tgc agc tat	1296
Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn Ala Gly Cys Ser Tyr	
420 425 430	
gtg aga ccc tcc cag tgg tca tcc atc cgc ctg tgg aca agc ccc acc	1344
Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu Trp Thr Ser Pro Thr	
435 440 445	
ttc cag tgg ctg atc ccc gac agc gct gac acc aca gct aca ccc acg	1392
Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr Thr Ala Thr Pro Thr	
450 455 460	
cac tgt gcc tat gac agg atc gtg gtt gca ggg atg ctg ctc cga ggg	1440
His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly Met Leu Leu Arg Gly	
465 470 475 480	
gcc gtt gtt ccc gac tcg gct ctt ccc ttt aac ttc cag gct gcc tat	1488
Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn Phe Gln Ala Ala Tyr	
485 490 495	
ggc ctg agt gac caa ctg gcc caa gcc atc agt gac cac tat cca gtg	1536
Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp His Tyr Pro Val	
500 505 510	
gag gtg atg ctg aag tga	1554
Glu Val Met Leu Lys	
515	

<210> 38

<211> 517

<212> PRT

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 38

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Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45

Ser Ala Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu

50		55		60
Glu Trp Val Gly Glu Ile Leu Pro Gly Ser Asn Asn Ser Arg Tyr Asn				
65		70		75
Glu Lys Phe Lys Gly Arg Val Thr Val Thr Arg Asp Thr Ser Thr Asn				
		85		90
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val				
		100		105
Tyr Tyr Cys Ala Arg Ser Tyr Asp Phe Ala Trp Phe Ala Tyr Trp Gly				
		115		120
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser				
		130		135
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala				
145		150		155
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val				
		165		170
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala				
		180		185
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val				
		195		200
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His				
		210		215
Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys				
225		230		235
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Gly Ser Gly				
		245		250
Gly Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr Phe Gly Glu Thr Lys				
		260		265
Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val Gln Ile Leu Ser Arg				
		275		280
				285

Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp Ser His Leu Thr Ala
 290 295 300
 Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp Ala Pro Asp Thr Tyr
 305 310 315 320
 His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn Ser Tyr Lys Glu Arg
 325 330 335
 Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser Ala Val Asp Ser Tyr
 340 345 350
 Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn Asp Thr Phe Asn Arg
 355 360 365
 Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe Thr Glu Val Arg Glu
 370 375 380
 Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly Asp Ala Val Ala Glu
 385 390 395 400
 Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val Gln Glu Lys Trp Gly
 405 410 415
 Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn Ala Gly Cys Ser Tyr
 420 425 430
 Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu Trp Thr Ser Pro Thr
 435 440 445
 Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr Thr Ala Thr Pro Thr
 450 455 460
 His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly Met Leu Leu Arg Gly
 465 470 475 480
 Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn Phe Gln Ala Ala Tyr
 485 490 495
 Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp His Tyr Pro Val
 500 505 510
 Glu Val Met Leu Lys
 515

<210> 39

<211> 1584

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 39

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tgcaaggctt ctggctacac cttcagtgcc tactggatag agtgggtgcg ccagggtcca      180
ggaaagggcc tcgagtgggt cggagagatt ttacctggaa gtaataattc tagatacaat      240
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aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt      720
gacaaaactc acacatgtcc accgtgtcca gcaccagagg ggagcggcgg gctgaagatc      780
gcagccttca acatccagac atttggggag accaagatgt ccaatgccac cctcgtcagc      840
tacattgtgc agatcctgag ccgctacgac atcgccctgg tccaggaggt cagagacagc      900
cacctgactg ccgtggggaa gctgctggac aacctcaatc aggacgcacc agacacctat      960
cactacgtgg tcagtgagec actgggacgg aacagctata aggagcgcta cctgttcgtg     1020
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gccgttggtc ccgactcggc tcttcctttt aacttccagg ctgcctatgg cctgagtgc 1500
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cccaaaaaga agcgcaaggt ttga 1584

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<210> 40

<211> 1584

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 40

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tgcaaggctt ctggctacac cttcagtgcc tactggatag agtgggtgcg ccaggctcca 180
ggaaagggcc tcgagtgggt cggagagatt ttacctggaa gtaataattc tagatacaat 240
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aagggcccat cggctcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg 480
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tacattgtgc agatcctgag ccgctacgac atcgccctgg tccaggaggt cagagacagc 900
cacctgactg ccgtggggaa gctgctggac aacctcaatc aggacgcacc agacacctat 960

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tgcgggaacg acaccttcaa ccgagagcca gccattgtca ggttcttctc ccggttcaca 1140
gaggtcaggg agtttgccat tgttcccctg catgcggccc cgggggacgc agtagccgag 1200
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gccgttggtc ccgactcggc tcttcccttt aacttccagg ctgcctatgg cctgagtgac 1500
caactggccc aagccatcag tgaccactat ccagtggagg tgatgctgaa ggggggcgga 1560
cccaaaaaga agcgcaaggt ttga 1584

```

<210> 41

<211> 1593

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 41

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cactcccagg tgcagctggg gcagtctggg gcagaggtga aaaagcctgg ggcctcagtg 120
aaggtgtcct gcaaggcttc tggctacacc ttcagtgcct actggataga gtgggtgctc 180
caggctccag gaaagggcct cgagtgggtc ggagagattt tacctggaag taataattct 240
agatacaatg agaagttcaa gggccgagtg acagtcacta gagacacatc cacaacaca 300
gcctacatgg agctcagcag cctgaggtct gaggacacag ccgtctatta ctgtgcaaga 360
tcctacgact ttgcctgggt tgcttactgg ggccaaggga ctctgggtcac agtctcctca 420
gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 480
ggcacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggt gacggtgtcg 540
tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 600
ggactctact ccctcagcag cgtgggtgacc gtgccctcca gcagcttggg caccagacc 660

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```

tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 720
aaatcttgtg acaaaactca cacatgtcca ccgtgtccag caccagaggg gagcggcggg 780
ctgaagatcg cagccttcaa catccagaca ttgggggaga ccaagatgtc caatgccacc 840
ctcgtcagct acattgtgca gatcctgagc cgctacgaca tcgccctggg ccaggagggtc 900
agagacagcc acctgactgc cgtggggaag ctgctggaca acctcaatca ggacgcacca 960
gacacctatc actacgtggg cagtgaagcca ctgggacgga acagctataa ggagcgctac 1020
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gtagccgaga tcgacgctct ctatgacgtc tacctggatg tccaagagaa atggggcttg 1260
gaggacgtca tggtgatggg cgacttcaat gcgggctgca gctatgtgag accctcccag 1320
tggtcatcca tccgcctgtg gacaagcccc accttccagt ggctgatccc cgacagcgct 1380
gacaccacag ctacaccac gcactgtgcc tatgacagga tcgtgggtgc agggatgctg 1440
ctccgagggg ccgttgttcc cgactcggct cttcccttta acttccaggc tgcctatggc 1500
ctgagtgacc aactggccca agccatcagt gaccactatc cagtggaggt gatgctgaag 1560
gggggcggac ccaaaaagaa gcgcaagggt tga 1593

```

<210> 42

<211> 1584

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<220>

<221> CDS

<222> (1) .. (1584)

<223>

<400> 42

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Met	Gly	Trp	Ser	Cys	Ile	Ile	Leu	Phe	Leu	Val	Ala	Thr	Ala	Thr	Gly	
1				5					10					15		
gtc	cac	tcc	cag	gtg	cag	ctg	gtg	cag	tct	ggg	gca	gag	gtg	aaa	aag	96
Val	His	Ser	Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	
			20					25					30			
cct	ggg	gcc	tca	gtg	aag	gtg	tcc	tgc	aag	gct	tct	ggc	tac	acc	ttc	144
Pro	Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	
		35					40					45				
agt	gcc	tac	tgg	ata	gag	tgg	gtg	cgc	cag	gct	cca	gga	aag	ggc	ctc	192
Ser	Ala	Tyr	Trp	Ile	Glu	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	
	50					55					60					
gag	tgg	gtc	gga	gag	att	tta	cct	gga	agt	aat	aat	tct	aga	tac	aat	240
Glu	Trp	Val	Gly	Glu	Ile	Leu	Pro	Gly	Ser	Asn	Asn	Ser	Arg	Tyr	Asn	
65					70				75						80	
gag	aag	ttc	aag	ggc	cga	gtg	aca	gtc	act	aga	gac	aca	tcc	aca	aac	288
Glu	Lys	Phe	Lys	Gly	Arg	Val	Thr	Val	Thr	Arg	Asp	Thr	Ser	Thr	Asn	
				85					90					95		
aca	gcc	tac	atg	gag	ctc	agc	agc	ctg	agg	tct	gag	gac	aca	gcc	gtc	336
Thr	Ala	Tyr	Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	
			100					105					110			
tat	tac	tgt	gca	aga	tcc	tac	gac	ttt	gcc	tgg	ttt	gct	tac	tgg	ggc	384
Tyr	Tyr	Cys	Ala	Arg	Ser	Tyr	Asp	Phe	Ala	Trp	Phe	Ala	Tyr	Trp	Gly	
		115					120					125				
caa	ggg	act	ctg	gtc	aca	gtc	tcc	tca	gcc	tcc	acc	aag	ggc	cca	tcg	432
Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	
	130					135					140					
gtc	ttc	ccc	ctg	gca	ccc	tcc	tcc	aag	agc	acc	tct	ggg	ggc	aca	gcg	480
Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	
145					150				155						160	
gcc	ctg	ggc	tgc	ctg	gtc	aag	gac	tac	ttc	ccc	gaa	ccg	gtg	acg	gtg	528
Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	
				165					170					175		
tcg	tgg	aac	tca	ggc	gcc	ctg	acc	agc	ggc	gtg	cac	acc	ttc	ccg	gct	576
Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	
			180					185					190			
gtc	cta	cag	tcc	tca	gga	ctc	tac	tcc	ctc	agc	agc	gtg	gtg	acc	gtg	624
Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	
		195					200					205				
ccc	tcc	agc	agc	ttg	ggc	acc	cag	acc	tac	atc	tgc	aac	gtg	aat	cac	672
Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	
	210					215					220					
aag	ccc	agc	aac	acc	aag	gtg	gac	aag	aaa	gtt	gag	ccc	aaa	tct	tgt	720
Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	
225					230					235					240	

gac Asp	aaa Lys	act Thr	cac His	aca Thr 245	tgc Cys	cca Pro	ccg Pro	tgc Cys	cca Pro 250	gca Ala	cct Pro	gaa Glu	ggg Gly	agc Ser 255	ggc Gly	768
ggg Gly	ctg Leu	aag Lys	atc Ile 260	gca Ala	gcc Ala	ttc Phe	aac Asn	atc Ile 265	cag Gln	aca Thr	ttt Phe	ggg Gly	gag Glu 270	acc Thr	aag Lys	816
atg Met	tcc Ser	aat Asn 275	gcc Ala	acc Thr	ctc Leu	gtc Val	agc Ser 280	tac Tyr	att Ile	gtg Val	cag Gln	atc Ile 285	ctg Leu	agc Ser	cgc Arg	864
tac Tyr	gac Asp 290	atc Ile	gcc Ala	ctg Leu	gtc Val	cag Gln 295	gag Glu	gtc Val	aga Arg	gac Asp	agc Ser 300	cac His	ctg Leu	act Thr	gcc Ala	912
gtg Val 305	ggg Gly	aag Lys	ctg Leu	ctg Leu	gac Asp 310	aac Asn	ctc Leu	aat Asn	cag Gln	gac Asp 315	gca Ala	cca Pro	gac Asp	acc Thr	tat Tyr 320	960
cac His	tac Tyr	gtg Val	gtc Val	agt Ser 325	gag Glu	cca Pro	ctg Leu	gga Gly	cgg Arg 330	aac Asn	agc Ser	tat Tyr	aag Lys	gag Glu 335	cgc Arg	1008
tac Tyr	ctg Leu	ttc Phe	gtg Val 340	tac Tyr	agg Arg	cct Pro	gac Asp	cag Gln	gtg Val	tct Ser	gcg Ala	gtg Val	gac Asp 350	agc Ser	tac Tyr	1056
tac Tyr	tac Tyr	gat Asp 355	gat Asp	ggc Gly	tgc Cys	gag Glu	ccc Pro 360	tgc Cys	ggg Gly	aac Asn	gac Asp	acc Thr 365	ttc Phe	aac Asn	cga Arg	1104
gag Glu 370	cca Pro	gcc Ala	att Ile	gtc Val	agg Arg	ttc Phe 375	ttc Phe	tcc Ser	cgg Arg	ttc Phe	aca Thr 380	gag Glu	gtc Val	agg Arg	gag Glu	1152
ttt Phe 385	gcc Ala	att Ile	gtt Val	ccc Pro	ctg Leu 390	cat His	gcg Ala	gcc Ala	ccg Pro	ggg Gly 395	gac Asp	gca Ala	gta Val	gcc Ala	gag Glu 400	1200
atc Ile	gac Asp	gct Ala	ctc Leu	tat Tyr 405	gac Asp	gtc Val	tac Tyr	ctg Leu	gat Asp 410	gtc Val	caa Gln	gag Glu	aaa Lys	tgg Trp 415	ggc Gly	1248
ttg Leu	gag Glu	gac Asp	gtc Val 420	atg Met	ttg Leu	atg Met	ggc Gly	gac Asp 425	ttc Phe	aat Asn	gcg Ala	ggc Gly	tgc Cys 430	agc Ser	tat Tyr	1296
gtg Val	aga Arg	ccc Pro 435	tcc Ser	cag Gln	tgg Trp	tca Ser	tcc Ser 440	atc Ile	cgc Arg	ctg Leu	tgg Trp	aca Thr 445	agc Ser	ccc Pro	acc Thr	1344
ttc Phe 450	cag Gln	tgg Trp	ctg Leu	atc Ile	ccc Pro	gac Asp 455	agc Ser	gct Ala	gac Asp	acc Thr	aca Thr 460	gct Ala	aca Thr	ccc Pro	acg Thr	1392
cac His	tgt Cys	gcc Ala	tat Tyr	gac Asp	agg Arg	atc Ile	gtg Val	gtt Val	gca Ala	ggg Gly	atg Met	ctg Leu	ctc Leu	cga Arg	ggg Gly	1440

465	470	475	480	
gcc gtt gtt ccc gac tcg gct ctt ccc ttt aac ttc cag gct gcc tat				1488
Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn Phe Gln Ala Ala Tyr				
	485	490	495	
ggc ctg agt gac caa ctg gcc caa gcc atc agt gac cac tat cca gtg				1536
Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp His Tyr Pro Val				
	500	505	510	
gag gtg atg ctg aag ggg ggc gga ccc aaa aag aag cgc aag gtt tga				1584
Glu Val Met Leu Lys Gly Gly Gly Pro Lys Lys Lys Arg Lys Val				
	515	520	525	

<210> 43

<211> 527

<212> PRT

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 43

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
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Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45

Ser Ala Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
50 55 60

Glu Trp Val Gly Glu Ile Leu Pro Gly Ser Asn Asn Ser Arg Tyr Asn
65 70 75 80

Glu Lys Phe Lys Gly Arg Val Thr Val Thr Arg Asp Thr Ser Thr Asn
85 90 95

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
100 105 110

Tyr	Tyr	Cys	Ala	Arg	Ser	Tyr	Asp	Phe	Ala	Trp	Phe	Ala	Tyr	Trp	Gly	115	120	125
Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	130	135	140
Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	145	150	155
Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	165	170	175
Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	180	185	190
Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	195	200	205
Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	210	215	220
Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	225	230	235
Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Gly	Ser	Gly	245	250	255
Gly	Leu	Lys	Ile	Ala	Ala	Phe	Asn	Ile	Gln	Thr	Phe	Gly	Glu	Thr	Lys	260	265	270
Met	Ser	Asn	Ala	Thr	Leu	Val	Ser	Tyr	Ile	Val	Gln	Ile	Leu	Ser	Arg	275	280	285
Tyr	Asp	Ile	Ala	Leu	Val	Gln	Glu	Val	Arg	Asp	Ser	His	Leu	Thr	Ala	290	295	300
Val	Gly	Lys	Leu	Leu	Asp	Asn	Leu	Asn	Gln	Asp	Ala	Pro	Asp	Thr	Tyr	305	310	315
His	Tyr	Val	Val	Ser	Glu	Pro	Leu	Gly	Arg	Asn	Ser	Tyr	Lys	Glu	Arg	325	330	335
Tyr	Leu	Phe	Val	Tyr	Arg	Pro	Asp	Gln	Val	Ser	Ala	Val	Asp	Ser	Tyr	340	345	350

Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn Asp Thr Phe Asn Arg
 355 360 365

Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe Thr Glu Val Arg Glu
 370 375 380

Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly Asp Ala Val Ala Glu
 385 390 395 400

Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val Gln Glu Lys Trp Gly
 405 410 415

Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn Ala Gly Cys Ser Tyr
 420 425 430

Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu Trp Thr Ser Pro Thr
 435 440 445

Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr Thr Ala Thr Pro Thr
 450 455 460

His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly Met Leu Leu Arg Gly
 465 470 475 480

Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn Phe Gln Ala Ala Tyr
 485 490 495

Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp His Tyr Pro Val
 500 505 510

Glu Val Met Leu Lys Gly Gly Gly Pro Lys Lys Lys Arg Lys Val
 515 520 525

<210> 44

<211> 2196

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 heavy chain - DNase I fusion

<400> 44
atgggatgga gctgtatcat cctcttcttg gtagcaacag ctacaggtgt ccactcccag 60
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tgcaaggctt ctggctacac cttcagtgcc tactggatag agtgggtgcg ccagggtcca 180
ggaaagggcc tcgagtgggt cggagagatt ttacctggaa gtaataattc tagatacaat 240
gagaagttca agggccgagt gacagtcact agagacacat ccacaaacac agcctacatg 300
gagctcagca gcctgaggtc tgaggacaca gccgtctatt actgtgcaag atcctacgac 360
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gccctggggt gcctgggtcaa ggactacttc cccgaaccgg tgacgggtgtc gtggaactca 540
ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac 600
tcctcagca gcgtggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc 660
aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt 720
gacaaaactc acacatgccc accgtgccc a gcacctgaac tcttgggggg accgtcagtc 780
ttctcttccc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca 840
tgcggtggtg tggacgtgag ccacgaagac cctgaggtca agttcaactg gtacgtggac 900
ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagtacaa cagcacgtac 960
cgtgtggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag 1020
tgcaaggctc ccaacaaagc cctcccagcc cccatcgaga aaaccatctc caaagccaaa 1080
gggcagcccc gagaaccaca ggtgtacacc ctgcccccat cccgggatga gctgaccaag 1140
aaccaggtca gcctgacctg cctgggtcaaa ggcttctatc ccagcgacat cgccgtggag 1200
tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccggt gctggactcc 1260
gacggctcct tcttctctta cagcaagctc accgtggaca agagcaggtg gcagcagggg 1320
aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc 1380
ctctccctgt ctccgggtaa agggagcggc gggctgaaga tcgcagcctt caacatccag 1440
acatttgggg agaccaagat gtccaatgcc accctcgtca gctacattgt gcagatcctg 1500
agccgctacg acatcgccct ggtccaggag gtcagagaca gccacctgac tgccgtgggg 1560
aagctgctgg acaacctcaa tcaggacgca ccagacacct atcactacgt ggtcagtgag 1620
ccactgggac ggaacagcta taaggagcgc tacctgttcg tgtacaggcc tgaccaggtg 1680
tctgcggtgg acagctacta ctacgatgat ggctgcgagc cctgcgggaa cgacaccttc 1740

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aaccgagagc cagccattgt cagggttcttc tcccgggttca cagaggtcag ggagtttgcc 1800
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gtctacctgg atgtccaaga gaaatggggc ttggaggacg tcatgttgat gggcgacttc 1920
aatgcgggct gcagctatgt gagaccctcc cagtgggtcat ccatccgcct gtggacaagc 1980
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gcctatgaca ggatcgtggt tgcagggatg ctgctccgag gggccgttgt tcccgactcg 2100
gctcttccct ttaacttcca ggctgcctat ggctgagtg accaactggc ccaagccatc 2160
agtgaccact atccagtgga ggtgatgctg aagtga 2196

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<210> 45

<211> 2196

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 heavy chain - DNase I fusion

<220>

<221> CDS

<222> (1)..(2196)

<223>

<400> 45

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1 5 10 15

gtc cac tcc cag gtg cag ctg gtg cag tct ggg gca gag gtg aaa aag 96
Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

cct ggg gcc tca gtg aag gtg tcc tgc aag gct tct ggc tac acc ttc 144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45

agt gcc tac tgg ata gag tgg gtg cgc cag gct cca gga aag ggc ctc 192
Ser Ala Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
50 55 60

gag tgg gtc gga gag att tta cct gga agt aat aat tct aga tac aat 240

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Glu 65	Trp	Val	Gly	Glu	Ile 70	Leu	Pro	Gly	Ser	Asn 75	Asn	Ser	Arg	Tyr	Asn 80	
gag Glu	aag Lys	ttc Phe	aag Lys	ggc Gly 85	cga Arg	gtg Val	aca Thr	gtc Val	act Thr 90	aga Arg	gac Asp	aca Thr	tcc Ser	aca Thr	aac Asn 95	288
aca Thr	gcc Ala	tac Tyr	atg Met 100	gag Glu	ctc Leu	agc Ser	agc Ser	ctg Leu 105	agg Arg	tct Ser	gag Glu	gac Asp	aca Thr	gcc Ala	gtc Val	336
tat Tyr	tac Tyr	tgt Cys 115	gca Ala	aga Arg	tcc Ser	tac Tyr	gac Asp 120	ttt Phe	gcc Ala	tgg Trp	ttt Phe	gct Ala 125	tac Tyr	tgg Trp	ggc Gly	384
caa Gln 130	ggg Gly	act Thr	ctg Leu	gtc Val	aca Thr	gtc Val 135	tcc Ser	tca Ser	gcc Ala	tcc Ser	acc Thr 140	aag Lys	ggc Gly	cca Pro	tcg Ser	432
gtc Val 145	ttc Phe	ccc Pro	ctg Leu	gca Ala	ccc Pro 150	tcc Ser	tcc Ser	aag Lys	agc Ser	acc Thr 155	tct Ser	ggg Gly	ggc Gly	aca Thr	gcg Ala 160	480
gcc Ala	ctg Leu	ggc Gly	tgc Cys 165	ctg Leu	gtc Val	aag Lys	gac Asp	tac Tyr	ttc Phe 170	ccc Pro	gaa Glu	ccg Pro	gtg Val	acg Thr	gtg Val	528
tcg Ser	tgg Trp	aac Asn 180	tca Ser	ggc Gly	gcc Ala	ctg Leu	acc Thr	agc Ser 185	ggc Gly	gtg Val	cac His	acc Thr	ttc Phe 190	ccg Pro	gct Ala	576
gtc Val	cta Leu	cag Gln 195	tcc Ser	tca Ser	gga Gly	ctc Leu	tac Tyr 200	tcc Ser	ctc Leu	agc Ser	agc Ser	gtg Val	gtg Val	acc Thr	gtg Val	624
ccc Pro 210	tcc Ser	agc Ser	agc Ser	ttg Leu	ggc Gly	acc Thr 215	cag Gln	acc Thr	tac Tyr	atc Ile	tgc Cys 220	aac Asn	gtg Val	aat Asn	cac His	672
aag Lys 225	ccc Pro	agc Ser	aac Asn	acc Thr	aag Lys 230	gtg Val	gac Asp	aag Lys	aaa Lys	gtt Val 235	gag Glu	ccc Pro	aaa Lys	tct Ser	tgt Cys 240	720
gac Asp	aaa Lys	act Thr	cac His 245	aca Thr	tgc Cys	cca Pro	ccg Pro	tgc Cys	cca Pro	gca Ala	cct Pro	gaa Glu	ctc Leu	ctg Leu	ggg Gly 255	768
gga Gly	ccg Pro	tca Ser	gtc Val	ttc Phe	ctc Leu	ttc Phe	ccc Pro	cca Pro	aaa Lys	ccc Pro	aag Lys	gac Asp	acc Thr	ctc Leu	atg Met	816
atc Ile	tcc Ser	cgg Arg 275	acc Thr	cct Pro	gag Glu	gtc Val	aca Thr 280	tgc Cys	gtg Val	gtg Val	gtg Val	gac Asp 285	gtg Val	agc Ser	cac His	864
gaa Glu 290	gac Asp	cct Pro	gag Glu	gtc Val	aag Lys	ttc Phe 295	aac Asn	tgg Trp	tac Tyr	gtg Val	gac Asp 300	ggc Gly	gtg Val	gag Glu	gtg Val	912

cat His 305	aat Asn	gcc Ala	aag Lys	aca Thr	aag Lys 310	ccg Pro	cgg Arg	gag Glu	gag Glu	cag Gln 315	tac Tyr	aac Asn	agc Ser	acg Thr	tac Tyr 320	960
cgt Arg	gtg Val	gtc Val	agc Ser	gtc Val 325	ctc Leu	acc Thr	gtc Val	ctg Leu	cac His 330	cag Gln	gac Asp	tgg Trp	ctg Leu	aat Asn 335	ggc Gly	1008
aag Lys	gag Glu	tac Tyr	aag Lys 340	tgc Cys	aag Lys	gtc Val	tcc Ser	aac Asn 345	aaa Lys	gcc Ala	ctc Leu	cca Pro	gcc Ala 350	ccc Pro	atc Ile	1056
gag Glu	aaa Lys	acc Thr 355	atc Ile	tcc Ser	aaa Lys	gcc Ala	aaa Lys 360	ggg Gly	cag Gln	ccc Pro	cga Arg	gaa Glu 365	cca Pro	cag Gln	gtg Val	1104
tac Tyr	acc Thr 370	ctg Leu	ccc Pro	cca Pro	tcc Ser	cgg Arg 375	gat Asp	gag Glu	ctg Leu	acc Thr	aag Lys 380	aac Asn	cag Gln	gtc Val	agc Ser	1152
ctg Leu 385	acc Thr	tgc Cys	ctg Leu	gtc Val	aaa Lys 390	ggc Gly	ttc Phe	tat Tyr	ccc Pro	agc Ser 395	gac Asp	atc Ile	gcc Ala	gtg Val	gag Glu 400	1200
tgg Trp	gag Glu	agc Ser	aat Asn	ggg Gly 405	cag Gln	ccg Pro	gag Glu	aac Asn 410	aac Asn	tac Tyr	aag Lys	acc Thr	acg Thr	cct Pro 415	ccc Pro	1248
gtg Val	ctg Leu	gac Asp	tcc Ser 420	gac Asp	ggc Gly	tcc Ser	ttc Phe	ttc Phe	ctc Leu	tac Tyr	agc Ser	aag Lys	ctc Leu 430	acc Thr	gtg Val	1296
gac Asp	aag Lys	agc Ser 435	agg Arg	tgg Trp	cag Gln	cag Gln	ggg Gly 440	aac Asn	gtc Val	ttc Phe	tca Ser	tgc Cys 445	tcc Ser	gtg Val	atg Met	1344
cat His 450	gag Glu	gct Ala	ctg Leu	cac His	aac Asn	cac His 455	tac Tyr	acg Thr	cag Gln	aag Lys	agc Ser	ctc Leu	tcc Ser	ctg Leu	tct Ser	1392
ccg Pro 465	ggt Gly	aaa Lys	ggg Gly	agc Ser	ggc Gly 470	ggg Gly	ctg Leu	aag Lys	atc Ile	gca Ala 475	gcc Ala	ttc Phe	aac Asn	atc Ile	cag Gln 480	1440
aca Thr	ttt Phe	ggg Gly	gag Glu	acc Thr 485	aag Lys	atg Met	tcc Ser	aat Asn	gcc Ala 490	acc Thr	ctc Leu	gtc Val	agc Ser	tac Tyr 495	att Ile	1488
gtg Val	cag Gln	atc Ile	ctg Leu	agc Ser	cgc Arg	tac Tyr	gac Asp	atc Ile	gcc Ala	ctg Leu	gtc Val	cag Gln	gag Glu	gtc Val	aga Arg	1536
gac Asp	agc Ser	cac His 515	ctg Leu	act Thr	gcc Ala	gtg Val	ggg Gly 520	aag Lys	ctg Leu	ctg Leu	gac Asp	aac Asn 525	ctc Leu	aat Asn	cag Gln	1584
gac Asp 530	gca Ala	cca Pro	gac Asp	acc Thr	tat Tyr	cac His 535	tac Tyr	gtg Val	gtc Val	agt Ser	gag Glu 540	cca Pro	ctg Leu	gga Gly	cgg Arg	1632

aac agc tat aag gag cgc tac ctg ttc gtg tac agg cct gac cag gtg Asn Ser Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val 545 550 555 560	1680
tct gcg gtg gac agc tac tac tac gat gat ggc tgc gag ccc tgc ggg Ser Ala Val Asp Ser Tyr Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly 565 570 575	1728
aac gac acc ttc aac cga gag cca gcc att gtc agg ttc ttc tcc cgg Asn Asp Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg 580 585 590	1776
ttc aca gag gtc agg gag ttt gcc att gtt ccc ctg cat gcg gcc ccg Phe Thr Glu Val Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro 595 600 605	1824
ggg gac gca gta gcc gag atc gac gct ctc tat gac gtc tac ctg gat Gly Asp Ala Val Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp 610 615 620	1872
gtc caa gag aaa tgg ggc ttg gag gac gtc atg ttg atg ggc gac ttc Val Gln Glu Lys Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe 625 630 635 640	1920
aat gcg ggc tgc agc tat gtg aga ccc tcc cag tgg tca tcc atc cgc Asn Ala Gly Cys Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg 645 650 655	1968
ctg tgg aca agc ccc acc ttc cag tgg ctg atc ccc gac agc gct gac Leu Trp Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp 660 665 670	2016
acc aca gct aca ccc acg cac tgt gcc tat gac agg atc gtg gtt gca Thr Thr Ala Thr Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala 675 680 685	2064
ggg atg ctg ctc cga ggg gcc gtt gtt ccc gac tcg gct ctt ccc ttt Gly Met Leu Leu Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe 690 695 700	2112
aac ttc cag gct gcc tat ggc ctg agt gac caa ctg gcc caa gcc atc Asn Phe Gln Ala Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile 705 710 715 720	2160
agt gac cac tat cca gtg gag gtg atg ctg aag tga Ser Asp His Tyr Pro Val Glu Val Met Leu Lys 725 730	2196

<210> 46

<211> 731

<212> PRT

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 heavy chain - DNase I fusion

<400> 46

Met	Gly	Trp	Ser	Cys	Ile	Ile	Leu	Phe	Leu	Val	Ala	Thr	Ala	Thr	Gly
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Val	His	Ser	Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys
			20					25					30		

Pro	Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe
		35					40					45			

Ser	Ala	Tyr	Trp	Ile	Glu	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu
	50					55					60				

Glu	Trp	Val	Gly	Glu	Ile	Leu	Pro	Gly	Ser	Asn	Asn	Ser	Arg	Tyr	Asn
65					70					75					80

Glu	Lys	Phe	Lys	Gly	Arg	Val	Thr	Val	Thr	Arg	Asp	Thr	Ser	Thr	Asn
				85					90					95	

Thr	Ala	Tyr	Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val
			100					105					110		

Tyr	Tyr	Cys	Ala	Arg	Ser	Tyr	Asp	Phe	Ala	Trp	Phe	Ala	Tyr	Trp	Gly
		115					120					125			

Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser
	130					135					140				

Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala
145					150					155					160

Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val
				165					170					175	

Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala
			180					185					190		

Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val
		195					200					205			

Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His
210						215					220				
Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys
225					230					235					240
Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly
				245					250					255	
Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met
			260					265					270		
Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His
		275					280					285			
Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val
	290					295					300				
His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr
305					310					315					320
Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly
				325					330					335	
Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile
			340					345					350		
Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val
		355					360					365			
Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser
	370					375					380				
Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu
385					390					395					400
Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro
				405					410					415	
Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val
			420					425					430		
Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met
		435					440					445			

His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	
450						455					460					
Pro	Gly	Lys	Gly	Ser	Gly	Gly	Leu	Lys	Ile	Ala	Ala	Phe	Asn	Ile	Gln	
465					470					475					480	
Thr	Phe	Gly	Glu	Thr	Lys	Met	Ser	Asn	Ala	Thr	Leu	Val	Ser	Tyr	Ile	
				485					490					495		
Val	Gln	Ile	Leu	Ser	Arg	Tyr	Asp	Ile	Ala	Leu	Val	Gln	Glu	Val	Arg	
			500					505					510			
Asp	Ser	His	Leu	Thr	Ala	Val	Gly	Lys	Leu	Leu	Asp	Asn	Leu	Asn	Gln	
		515					520					525				
Asp	Ala	Pro	Asp	Thr	Tyr	His	Tyr	Val	Val	Ser	Glu	Pro	Leu	Gly	Arg	
	530					535					540					
Asn	Ser	Tyr	Lys	Glu	Arg	Tyr	Leu	Phe	Val	Tyr	Arg	Pro	Asp	Gln	Val	
545					550					555					560	
Ser	Ala	Val	Asp	Ser	Tyr	Tyr	Tyr	Asp	Asp	Gly	Cys	Glu	Pro	Cys	Gly	
				565					570					575		
Asn	Asp	Thr	Phe	Asn	Arg	Glu	Pro	Ala	Ile	Val	Arg	Phe	Phe	Ser	Arg	
			580					585					590			
Phe	Thr	Glu	Val	Arg	Glu	Phe	Ala	Ile	Val	Pro	Leu	His	Ala	Ala	Pro	
		595					600					605				
Gly	Asp	Ala	Val	Ala	Glu	Ile	Asp	Ala	Leu	Tyr	Asp	Val	Tyr	Leu	Asp	
	610					615					620					
Val	Gln	Glu	Lys	Trp	Gly	Leu	Glu	Asp	Val	Met	Leu	Met	Gly	Asp	Phe	
625					630					635					640	
Asn	Ala	Gly	Cys	Ser	Tyr	Val	Arg	Pro	Ser	Gln	Trp	Ser	Ser	Ile	Arg	
				645					650					655		
Leu	Trp	Thr	Ser	Pro	Thr	Phe	Gln	Trp	Leu	Ile	Pro	Asp	Ser	Ala	Asp	
			660					665					670			
Thr	Thr	Ala	Thr	Pro	Thr	His	Cys	Ala	Tyr	Asp	Arg	Ile	Val	Val	Ala	

675

680

685

Gly Met Leu Leu Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe
 690 695 700

Asn Phe Gln Ala Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile
 705 710 715 720

Ser Asp His Tyr Pro Val Glu Val Met Leu Lys
 725 730

<210> 47

<211> 2193

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 heavy chain - DNase I fusion

<400> 47

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gtgcagctgg tgcagtctgg ggcagaggtg aaaaagcctg gggcctcagt gaaggtgtcc	120
tgcaaggctt ctggctacac cttcagtgcc tactggatag agtgggtgcg ccaggctcca	180
ggaaagggcc tcgagtgggt cggagagatt ttacctggaa gtaataattc tagatacaat	240
gagaagttca agggccgagt gacagtcact agagacacat ccacaaacac agcctacatg	300
gagctcagca gcctgaggtc tgaggacaca gccgtctatt actgtgcaag atcctacgac	360
tttgcttggg ttgcttactg gggccaaggg actctgggtca cagtctcctc agcctccacc	420
aaggggccat cggctcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg	480
gccctggggt gcctgggtcaa ggactacttc cccgaaccgg tgacgggtgtc gtggaactca	540
ggcgccctga ccagcggcgt gcacaccttc ccgggtgtcc tacagtcctc aggactctac	600
tcctcagca gcgtgggtgac cgtgccctcc agcagcttgg gcaccacagac ctacatctgc	660
aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt	720
gacaaaactc acacatgccc accgtgccc gcacctgaac tcctgggggg accgtcagtc	780
ttcctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca	840
tgcggtgggtg tggacgtgag ccacgaagac cctgaggtca agttcaactg gtacgtggac	900

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ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagtacaa cagcacgtac      960
cgtgtgggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag    1020
tgcaaggtct ccaacaaagc cctcccagcc cccatcgaga aaaccatctc caaagccaaa    1080
gggcagcccc gagaaccaca ggtgtacacc ctgcccccat cccgggatga gctgaccaag    1140
aaccagggtca gcctgacctg cctgggtcaaa ggcttctatc ccagcgacat cgccgtggag    1200
tgggagagca atgggcagcc ggagaacaac tacaagacca cgctcccgt gctggactcc    1260
gacggctcct tcttcctcta cagcaagctc accgtggaca agagcagggtg gcagcagggg    1320
aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc    1380
ctctccctgt ctccgaaggg gagcggcggg ctgaagatcg cagccttcaa catccagaca    1440
tttggggaga ccaagatgtc caatgccacc ctcgtcagct acattgtgca gatcctgagc    1500
cgctacgaca tcgccctggt ccaggaggtc agagacagcc acctgactgc cgtggggaag    1560
ctgctggaca acctcaatca ggacgcacca gacacctatc actacgtggg cagtgaacca    1620
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cgagagccag ccattgtcag gttcttctcc cggttcacag aggtcaggga gtttgccatt    1800
gttcccctgc atgcggcccc gggggacgca gtagccgaga tcgacgctct ctatgacgtc    1860
tacctggatg tccaagagaa atggggcttg gaggacgtca tggtgatggg cgacttcaat    1920
gcgggctgca gctatgtgag accctcccag tggatcatcca tccgcctgtg gacaagcccc    1980
accttccagt ggctgatccc cgacagcgct gacaccacag ctacaccac gcactgtgcc    2040
tatgacagga tcgtggttgc agggatgctg ctccgagggg ccgttggtcc cgactcggct    2100
cttcccttta acttccaggc tgcctatggc ctgagtgacc aactggccca agccatcagt    2160
gaccactatc cagtggaggt gatgctgaag tga                                  2193

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<210> 48

<211> 2193

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 heavy chain - DNase I fusion

<220>

<221> CDS

<222> (1)..(2193)

<223>

<400> 48

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Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly	
1 5 10 15	
gtc cac tcc cag gtg cag ctg gtg cag tct ggg gca gag gtg aaa aag	96
Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys	
20 25 30	
cct ggg gcc tca gtg aag gtg tcc tgc aag gct tct ggc tac acc ttc	144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe	
35 40 45	
agt gcc tac tgg ata gag tgg gtg cgc cag gct cca gga aag ggc ctc	192
Ser Ala Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu	
50 55 60	
gag tgg gtc gga gag att tta cct gga agt aat aat tct aga tac aat	240
Glu Trp Val Gly Glu Ile Leu Pro Gly Ser Asn Asn Ser Arg Tyr Asn	
65 70 75 80	
gag aag ttc aag ggc cga gtg aca gtc act aga gac aca tcc aca aac	288
Glu Lys Phe Lys Gly Arg Val Thr Val Thr Arg Asp Thr Ser Thr Asn	
85 90 95	
aca gcc tac atg gag ctc agc agc ctg agg tct gag gac aca gcc gtc	336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val	
100 105 110	
tat tac tgt gca aga tcc tac gac ttt gcc tgg ttt gct tac tgg ggc	384
Tyr Tyr Cys Ala Arg Ser Tyr Asp Phe Ala Trp Phe Ala Tyr Trp Gly	
115 120 125	
caa ggg act ctg gtc aca gtc tcc tca gcc tcc acc aag ggc cca tcg	432
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser	
130 135 140	
gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg	480
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala	
145 150 155 160	
gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg	528
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val	
165 170 175	
tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct	576
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala	
180 185 190	

gtc	cta	cag	tcc	tca	gga	ctc	tac	tcc	ctc	agc	agc	gtg	gtg	acc	gtg	624
Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	
		195					200					205				
ccc	tcc	agc	agc	ttg	ggc	acc	cag	acc	tac	atc	tgc	aac	gtg	aat	cac	672
Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	
	210					215					220					
aag	ccc	agc	aac	acc	aag	gtg	gac	aag	aaa	gtt	gag	ccc	aaa	tct	tgt	720
Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	
225					230					235					240	
gac	aaa	act	cac	aca	tgc	cca	ccg	tgc	cca	gca	cct	gaa	ctc	ctg	ggg	768
Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	
				245					250					255		
gga	ccg	tca	gtc	ttc	ctc	ttc	ccc	cca	aaa	ccc	aag	gac	acc	ctc	atg	816
Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	
			260				265						270			
atc	tcc	cgg	acc	cct	gag	gtc	aca	tgc	gtg	gtg	gtg	gac	gtg	agc	cac	864
Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	
		275					280					285				
gaa	gac	cct	gag	gtc	aag	ttc	aac	tgg	tac	gtg	gac	ggc	gtg	gag	gtg	912
Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	
	290					295					300					
cat	aat	gcc	aag	aca	aag	ccg	cgg	gag	gag	cag	tac	aac	agc	acg	tac	960
His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	
305					310					315					320	
cgt	gtg	gtc	agc	gtc	ctc	acc	gtc	ctg	cac	cag	gac	tgg	ctg	aat	ggc	1008
Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	
				325					330					335		
aag	gag	tac	aag	tgc	aag	gtc	tcc	aac	aaa	gcc	ctc	cca	gcc	ccc	atc	1056
Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	
			340				345					350				
gag	aaa	acc	atc	tcc	aaa	gcc	aaa	ggg	cag	ccc	cga	gaa	cca	cag	gtg	1104
Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	
		355				360					365					
tac	acc	ctg	ccc	cca	tcc	cgg	gat	gag	ctg	acc	aag	aac	cag	gtc	agc	1152
Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	
	370					375					380					
ctg	acc	tgc	ctg	gtc	aaa	ggc	ttc	tat	ccc	agc	gac	atc	gcc	gtg	gag	1200
Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	
385					390					395					400	
tgg	gag	agc	aat	ggg	cag	ccg	gag	aac	aac	tac	aag	acc	acg	cct	ccc	1248
Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	
				405				410						415		
gtg	ctg	gac	tcc	gac	ggc	tcc	ttc	ttc	ctc	tac	agc	aag	ctc	acc	gtg	1296
Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	

420	425	430	
gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met 435 440 445			1344
cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg tct His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser 450 455 460			1392
ccg aag ggg agc ggc ggg ctg aag atc gca gcc ttc aac atc cag aca Pro Lys Gly Ser Gly Gly Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr 465 470 475 480			1440
ttt ggg gag acc aag atg tcc aat gcc acc ctc gtc agc tac att gtg Phe Gly Glu Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val 485 490 495			1488
cag atc ctg agc cgc tac gac atc gcc ctg gtc cag gag gtc aga gac Gln Ile Leu Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp 500 505 510			1536
agc cac ctg act gcc gtg ggg aag ctg ctg gac aac ctc aat cag gac Ser His Leu Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp 515 520 525			1584
gca cca gac acc tat cac tac gtg gtc agt gag cca ctg gga cgg aac Ala Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn 530 535 540			1632
agc tat aag gag cgc tac ctg ttc gtg tac agg cct gac cag gtg tct Ser Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser 545 550 555 560			1680
gcg gtg gac agc tac tac tac gat gat ggc tgc gag ccc tgc ggg aac Ala Val Asp Ser Tyr Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn 565 570 575			1728
gac acc ttc aac cga gag cca gcc att gtc agg ttc ttc tcc cgg ttc Asp Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe 580 585 590			1776
aca gag gtc agg gag ttt gcc att gtt ccc ctg cat gcg gcc ccg ggg Thr Glu Val Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly 595 600 605			1824
gac gca gta gcc gag atc gac gct ctc tat gac gtc tac ctg gat gtc Asp Ala Val Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val 610 615 620			1872
caa gag aaa tgg ggc ttg gag gac gtc atg ttg atg ggc gac ttc aat Gln Glu Lys Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn 625 630 635 640			1920
gcg ggc tgc agc tat gtg aga ccc tcc cag tgg tca tcc atc cgc ctg Ala Gly Cys Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu 645 650 655			1968
tgg aca agc ccc acc ttc cag tgg ctg atc ccc gac agc gct gac acc			2016

Trp	Thr	Ser	Pro	Thr	Phe	Gln	Trp	Leu	Ile	Pro	Asp	Ser	Ala	Asp	Thr		
			660					665					670				
aca	gct	aca	ccc	acg	cac	tgt	gcc	tat	gac	agg	atc	gtg	ggt	gca	ggg	2064	
Thr	Ala	Thr	Pro	Thr	His	Cys	Ala	Tyr	Asp	Arg	Ile	Val	Val	Ala	Gly		
			675				680					685					
atg	ctg	ctc	cga	ggg	gcc	gtt	gtt	ccc	gac	tcg	gct	ctt	ccc	ttt	aac	2112	
Met	Leu	Leu	Arg	Gly	Ala	Val	Val	Pro	Asp	Ser	Ala	Leu	Pro	Phe	Asn		
	690					695					700						
ttc	cag	gct	gcc	tat	ggc	ctg	agt	gac	caa	ctg	gcc	caa	gcc	atc	agt	2160	
Phe	Gln	Ala	Ala	Tyr	Gly	Leu	Ser	Asp	Gln	Leu	Ala	Gln	Ala	Ile	Ser		
705					710					715					720		
gac	cac	tat	cca	gtg	gag	gtg	atg	ctg	aag	tga						2193	
Asp	His	Tyr	Pro	Val	Glu	Val	Met	Leu	Lys								
				725					730								

<210> 49

<211> 730

<212> PRT

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 heavy chain - DNase I fusion

<400> 49

Met	Gly	Trp	Ser	Cys	Ile	Ile	Leu	Phe	Leu	Val	Ala	Thr	Ala	Thr	Gly		
1				5					10					15			
Val	His	Ser	Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys		
			20					25					30				
Pro	Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe		
		35					40					45					
Ser	Ala	Tyr	Trp	Ile	Glu	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu		
	50					55					60						
Glu	Trp	Val	Gly	Glu	Ile	Leu	Pro	Gly	Ser	Asn	Asn	Ser	Arg	Tyr	Asn		
65					70					75					80		
Glu	Lys	Phe	Lys	Gly	Arg	Val	Thr	Val	Thr	Arg	Asp	Thr	Ser	Thr	Asn		
				85					90						95		

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
 100 105 110

Tyr Tyr Cys Ala Arg Ser Tyr Asp Phe Ala Trp Phe Ala Tyr Trp Gly
 115 120 125

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
 130 135 140

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
 145 150 155 160

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
 165 170 175

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
 180 185 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
 195 200 205

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
 210 215 220

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
 225 230 235 240

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 245 250 255

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
 260 265 270

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
 275 280 285

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
 290 295 300

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
 305 310 315 320

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
 325 330 335

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
 340 345 350
 Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
 355 360 365
 Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
 370 375 380
 Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
 385 390 395 400
 Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
 405 410 415
 Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
 420 425 430
 Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
 435 440 445
 His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
 450 455 460
 Pro Lys Gly Ser Gly Gly Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr
 465 470 475 480
 Phe Gly Glu Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val
 485 490 495
 Gln Ile Leu Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp
 500 505 510
 Ser His Leu Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp
 515 520 525
 Ala Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn
 530 535 540
 Ser Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser
 545 550 555 560
 Ala Val Asp Ser Tyr Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn

				565						570					575
Asp	Thr	Phe	Asn	Arg	Glu	Pro	Ala	Ile	Val	Arg	Phe	Phe	Ser	Arg	Phe
			580					585					590		
Thr	Glu	Val	Arg	Glu	Phe	Ala	Ile	Val	Pro	Leu	His	Ala	Ala	Pro	Gly
		595					600					605			
Asp	Ala	Val	Ala	Glu	Ile	Asp	Ala	Leu	Tyr	Asp	Val	Tyr	Leu	Asp	Val
	610					615					620				
Gln	Glu	Lys	Trp	Gly	Leu	Glu	Asp	Val	Met	Leu	Met	Gly	Asp	Phe	Asn
625					630					635					640
Ala	Gly	Cys	Ser	Tyr	Val	Arg	Pro	Ser	Gln	Trp	Ser	Ser	Ile	Arg	Leu
				645					650					655	
Trp	Thr	Ser	Pro	Thr	Phe	Gln	Trp	Leu	Ile	Pro	Asp	Ser	Ala	Asp	Thr
			660					665					670		
Thr	Ala	Thr	Pro	Thr	His	Cys	Ala	Tyr	Asp	Arg	Ile	Val	Val	Ala	Gly
		675					680					685			
Met	Leu	Leu	Arg	Gly	Ala	Val	Val	Pro	Asp	Ser	Ala	Leu	Pro	Phe	Asn
	690					695					700				
Phe	Gln	Ala	Ala	Tyr	Gly	Leu	Ser	Asp	Gln	Leu	Ala	Gln	Ala	Ile	Ser
705					710					715					720
Asp	His	Tyr	Pro	Val	Glu	Val	Met	Leu	Lys						
				725					730						

<210> 50

<211> 2190

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 heavy chain - DNase I fusion

<400> 50

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60

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tgcaaggctt ctggctacac cttcagtgcc tactggatag agtgggtgcg ccaggctcca	180
ggaaagggcc tcgagtgggt cggagagatt ttacctggaa gtaataattc tagatacaat	240
gagaagttca agggccgagt gacagtcact agagacacat ccacaaacac agcctacatg	300
gagctcagca gcctgaggtc tgaggacaca gccgtctatt actgtgcaag atcctacgac	360
tttgccctgg tttgcttactg gggccaaggg actctgggtca cagtctcctc agcctccacc	420
aaggggcccat cggctcttccc cctggcacc cctccaaga gcacctctgg gggcacagcg	480
gccctgggct gcctgggtcaa ggactacttc cccgaaccgg tgacgggtgtc gtggaactca	540
ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac	600
tccctcagca gcgtgggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc	660
aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt	720
gacaaaactc acacatgccc accgtgccc gcacctgaac tcctgggggg accgtcagtc	780
ttcctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca	840
tgcgtgggtg tggacgtgag ccacgaagac cctgaggtca agttcaactg gtacgtggac	900
ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagtacaa cagcacgtac	960
cgtgtgggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag	1020
tgcaagggtc ccaacaaagc cctcccagcc cccatcgaga aaaccatctc caaagccaaa	1080
gggcagcccc gagaaccaca ggtgtacacc ctgcccccat cccgggatga gctgaccaag	1140
aaccaggtca gcctgacctg cctgggtcaaa ggcttctatc ccagcgacat cgcctggag	1200
tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc	1260
gacggctcct tcttcctcta cagcaagctc accgtggaca agagcaggtg gcagcagggg	1320
aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc	1380
ctctccctgt ccccggggag cggcggggtg aagatcgag ccttcaacat ccagacattt	1440
ggggagacca agatgtccaa tgccaccctc gtcagctaca ttgtgcagat cctgagccgc	1500
tacgacatcg ccctgggtcca ggaggtcaga gacagccacc tgactgccgt ggggaagctg	1560
ctggacaacc tcaatcagga cgcaccagac acctatcact acgtgggtcag tgagccactg	1620
ggacggaaca gctataagga gcgctacctg ttcgtgtaca ggcctgacca ggtgtctgcg	1680
gtggacagct actactacga tgatgggtgc gagccctgcg ggaacgacac cttcaaccga	1740
gagccagcca ttgtcaggtt cttctcccgg ttcacagagg tcagggagtt tgccattgtt	1800

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cccctgcatg cggccccggg ggacgcagta gccgagatcg acgctctcta tgacgtctac 1860
ctggatgtcc aagagaaatg gggcttggag gacgtcatgt tgatgggcga cttcaatgcg 1920
ggctgcagct atgtgagacc ctcccagtgg tcatccatcc gcctgtggac aagccccacc 1980
ttccagtggc tgatccccga cagcgtgac accacagcta caccacgca ctgtgcctat 2040
gacaggatcg tggttgcagg gatgctgctc cgagggggccg ttgttcccga ctcggtcttt 2100
ccctttaact tccaggctgc ctatggcctg agtgaccaac tggcccaagc catcagtgac 2160
cactatccag tggaggtgat gctgaagtga 2190

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<210> 51

<211> 2190

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 heavy chain - DNase I fusion

<220>

<221> CDS

<222> (1)..(2190)

<223>

<400> 51

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Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1 5 10 15

gtc cac tcc cag gtg cag ctg gtg cag tct ggg gca gag gtg aaa aag 96
Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

cct ggg gcc tca gtg aag gtg tcc tgc aag gct tct ggc tac acc ttc 144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45

agt gcc tac tgg ata gag tgg gtg cgc cag gct cca gga aag ggc ctc 192
Ser Ala Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
50 55 60

gag tgg gtc gga gag att tta cct gga agt aat aat tct aga tac aat 240
Glu Trp Val Gly Glu Ile Leu Pro Gly Ser Asn Asn Ser Arg Tyr Asn
65 70 75 80

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gag	aag	ttc	aag	ggc	cga	gtg	aca	gtc	act	aga	gac	aca	tcc	aca	aac	288
Glu	Lys	Phe	Lys	Gly	Arg	Val	Thr	Val	Thr	Arg	Asp	Thr	Ser	Thr	Asn	
				85					90					95		
aca	gcc	tac	atg	gag	ctc	agc	agc	ctg	agg	tct	gag	gac	aca	gcc	gtc	336
Thr	Ala	Tyr	Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	
			100					105					110			
tat	tac	tgt	gca	aga	tcc	tac	gac	ttt	gcc	tgg	ttt	gct	tac	tgg	ggc	384
Tyr	Tyr	Cys	Ala	Arg	Ser	Tyr	Asp	Phe	Ala	Trp	Phe	Ala	Tyr	Trp	Gly	
		115					120					125				
caa	ggg	act	ctg	gtc	aca	gtc	tcc	tca	gcc	tcc	acc	aag	ggc	cca	tcg	432
Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	
	130					135					140					
gtc	ttc	ccc	ctg	gca	ccc	tcc	tcc	aag	agc	acc	tct	ggg	ggc	aca	gcg	480
Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	
145					150					155					160	
gcc	ctg	ggc	tgc	ctg	gtc	aag	gac	tac	ttc	ccc	gaa	ccg	gtg	acg	gtg	528
Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	
				165					170					175		
tcg	tgg	aac	tca	ggc	gcc	ctg	acc	agc	ggc	gtg	cac	acc	ttc	ccg	gct	576
Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	
			180					185					190			
gtc	cta	cag	tcc	tca	gga	ctc	tac	tcc	ctc	agc	agc	gtg	gtg	acc	gtg	624
Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	
		195					200					205				
ccc	tcc	agc	agc	ttg	ggc	acc	cag	acc	tac	atc	tgc	aac	gtg	aat	cac	672
Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	
	210					215					220					
aag	ccc	agc	aac	acc	aag	gtg	gac	aag	aaa	gtt	gag	ccc	aaa	tct	tgt	720
Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	
225					230					235					240	
gac	aaa	act	cac	aca	tgc	cca	ccg	tgc	cca	gca	cct	gaa	ctc	ctg	ggg	768
Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	
				245					250					255		
gga	ccg	tca	gtc	ttc	ctc	ttc	ccc	cca	aaa	ccc	aag	gac	acc	ctc	atg	816
Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	
			260					265					270			
atc	tcc	cgg	acc	cct	gag	gtc	aca	tgc	gtg	gtg	gtg	gac	gtg	agc	cac	864
Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	
		275					280					285				
gaa	gac	cct	gag	gtc	aag	ttc	aac	tgg	tac	gtg	gac	ggc	gtg	gag	gtg	912
Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	
	290					295					300					
cat	aat	gcc	aag	aca	aag	ccg	cgg	gag	gag	cag	tac	aac	agc	acg	tac	960
His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	

305					310					315					320	
cgt	gtg	gtc	agc	gtc	ctc	acc	gtc	ctg	cac	cag	gac	tgg	ctg	aat	ggc	1008
Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	
				325					330					335		
aag	gag	tac	aag	tgc	aag	gtc	tcc	aac	aaa	gcc	ctc	cca	gcc	ccc	atc	1056
Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	
			340					345					350			
gag	aaa	acc	atc	tcc	aaa	gcc	aaa	ggg	cag	ccc	cga	gaa	cca	cag	gtg	1104
Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	
		355					360					365				
tac	acc	ctg	ccc	cca	tcc	cgg	gat	gag	ctg	acc	aag	aac	cag	gtc	agc	1152
Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	
	370					375					380					
ctg	acc	tgc	ctg	gtc	aaa	ggc	ttc	tat	ccc	agc	gac	atc	gcc	gtg	gag	1200
Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	
385					390					395					400	
tgg	gag	agc	aat	ggg	cag	ccg	gag	aac	aac	tac	aag	acc	acg	cct	ccc	1248
Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	
			405					410						415		
gtg	ctg	gac	tcc	gac	ggc	tcc	ttc	ttc	ctc	tac	agc	aag	ctc	acc	gtg	1296
Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	
			420				425						430			
gac	aag	agc	agg	tgg	cag	cag	ggg	aac	gtc	ttc	tca	tgc	tcc	gtg	atg	1344
Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	
		435					440					445				
cat	gag	gct	ctg	cac	aac	cac	tac	acg	cag	aag	agc	ctc	tcc	ctg	tcc	1392
His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	
	450					455					460					
ccg	ggg	agc	ggc	ggg	ctg	aag	atc	gca	gcc	ttc	aac	atc	cag	aca	ttt	1440
Pro	Gly	Ser	Gly	Gly	Leu	Lys	Ile	Ala	Ala	Phe	Asn	Ile	Gln	Thr	Phe	
465					470					475					480	
ggg	gag	acc	aag	atg	tcc	aat	gcc	acc	ctc	gtc	agc	tac	att	gtg	cag	1488
Gly	Glu	Thr	Lys	Met	Ser	Asn	Ala	Thr	Leu	Val	Ser	Tyr	Ile	Val	Gln	
			485					490					495			
atc	ctg	agc	cgc	tac	gac	atc	gcc	ctg	gtc	cag	gag	gtc	aga	gac	agc	1536
Ile	Leu	Ser	Arg	Tyr	Asp	Ile	Ala	Leu	Val	Gln	Glu	Val	Arg	Asp	Ser	
			500					505					510			
cac	ctg	act	gcc	gtg	ggg	aag	ctg	ctg	gac	aac	ctc	aat	cag	gac	gca	1584
His	Leu	Thr	Ala	Val	Gly	Lys	Leu	Leu	Asp	Asn	Leu	Asn	Gln	Asp	Ala	
		515					520					525				
cca	gac	acc	tat	cac	tac	gtg	gtc	agt	gag	cca	ctg	gga	cgg	aac	agc	1632
Pro	Asp	Thr	Tyr	His	Tyr	Val	Val	Ser	Glu	Pro	Leu	Gly	Arg	Asn	Ser	
	530					535					540					
tat	aag	gag	cgc	tac	ctg	ttc	gtg	tac	agg	cct	gac	cag	gtg	tct	gcg	1680

Tyr 545	Lys	Glu	Arg	Tyr	Leu 550	Phe	Val	Tyr	Arg	Pro 555	Asp	Gln	Val	Ser	Ala 560	
gtg	gac	agc	tac	tac	tac	gat	gat	ggc	tgc	gag	ccc	tgc	ggg	aac	gac	1728
Val	Asp	Ser	Tyr	Tyr	Tyr	Asp	Asp	Gly	Cys 570	Glu	Pro	Cys	Gly	Asn 575	Asp	
acc	ttc	aac	cga	gag	cca	gcc	att	gtc	agg	ttc	ttc	tcc	cgg	ttc	aca	1776
Thr	Phe	Asn	Arg	Glu	Pro	Ala	Ile	Val	Arg	Phe	Phe	Ser	Arg	Phe	Thr	
			580					585					590			
gag	gtc	agg	gag	ttt	gcc	att	gtt	ccc	ctg	cat	gcg	gcc	ccg	ggg	gac	1824
Glu	Val	Arg	Glu	Phe	Ala	Ile	Val	Pro	Leu	His	Ala	Ala	Pro	Gly	Asp	
		595					600					605				
gca	gta	gcc	gag	atc	gac	gct	ctc	tat	gac	gtc	tac	ctg	gat	gtc	caa	1872
Ala	Val	Ala	Glu	Ile	Asp	Ala	Leu	Tyr	Asp	Val	Tyr	Leu	Asp	Val	Gln	
	610					615					620					
gag	aaa	tgg	ggc	ttg	gag	gac	gtc	atg	ttg	atg	ggc	gac	ttc	aat	gcg	1920
Glu	Lys	Trp	Gly	Leu	Glu	Asp	Val	Met	Leu	Met	Gly	Asp	Phe	Asn	Ala	
625					630				635						640	
ggc	tgc	agc	tat	gtg	aga	ccc	tcc	cag	tgg	tca	tcc	atc	cgc	ctg	tgg	1968
Gly	Cys	Ser	Tyr	Val	Arg	Pro	Ser	Gln	Trp	Ser	Ser	Ile	Arg	Leu	Trp	
				645				650						655		
aca	agc	ccc	acc	ttc	cag	tgg	ctg	atc	ccc	gac	agc	gct	gac	acc	aca	2016
Thr	Ser	Pro	Thr	Phe	Gln	Trp	Leu	Ile	Pro	Asp	Ser	Ala	Asp	Thr	Thr	
			660					665					670			
gct	aca	ccc	acg	cac	tgt	gcc	tat	gac	agg	atc	gtg	gtt	gca	ggg	atg	2064
Ala	Thr	Pro	Thr	His	Cys	Ala	Tyr	Asp	Arg	Ile	Val	Val	Ala	Gly	Met	
		675					680					685				
ctg	ctc	cga	ggg	gcc	gtt	gtt	ccc	gac	tcg	gct	ctt	ccc	ttt	aac	ttc	2112
Leu	Leu	Arg	Gly	Ala	Val	Val	Pro	Asp	Ser	Ala	Leu	Pro	Phe	Asn	Phe	
	690					695					700					
cag	gct	gcc	tat	ggc	ctg	agt	gac	caa	ctg	gcc	caa	gcc	atc	agt	gac	2160
Gln	Ala	Ala	Tyr	Gly	Leu	Ser	Asp	Gln	Leu	Ala	Gln	Ala	Ile	Ser	Asp	
705					710				715						720	
cac	tat	cca	gtg	gag	gtg	atg	ctg	aag	tga							2190
His	Tyr	Pro	Val	Glu	Val	Met	Leu	Lys								
				725												

<210> 52

<211> 729

<212> PRT

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 heavy chain - DNase I fusion

<400> 52

Met	Gly	Trp	Ser	Cys	Ile	Ile	Leu	Phe	Leu	Val	Ala	Thr	Ala	Thr	Gly
1				5					10					15	

Val	His	Ser	Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys
			20					25					30		

Pro	Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe
		35					40					45			

Ser	Ala	Tyr	Trp	Ile	Glu	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu
	50					55					60				

Glu	Trp	Val	Gly	Glu	Ile	Leu	Pro	Gly	Ser	Asn	Asn	Ser	Arg	Tyr	Asn
65					70					75					80

Glu	Lys	Phe	Lys	Gly	Arg	Val	Thr	Val	Thr	Arg	Asp	Thr	Ser	Thr	Asn
				85					90					95	

Thr	Ala	Tyr	Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val
			100					105					110		

Tyr	Tyr	Cys	Ala	Arg	Ser	Tyr	Asp	Phe	Ala	Trp	Phe	Ala	Tyr	Trp	Gly
		115					120					125			

Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser
	130					135					140				

Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala
145					150					155					160

Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val
			165						170					175	

Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala
		180						185					190		

Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val
		195					200					205			

Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

210					215					220					
Lys 225	Pro	Ser	Asn	Thr	Lys 230	Val	Asp	Lys	Lys	Val	Glu 235	Pro	Lys	Ser	Cys 240
Asp	Lys	Thr	His	Thr 245	Cys	Pro	Pro	Cys	Pro 250	Ala	Pro	Glu	Leu	Leu	Gly 255
Gly	Pro	Ser	Val 260	Phe	Leu	Phe	Pro	Pro 265	Lys	Pro	Lys	Asp	Thr 270	Leu	Met
Ile	Ser 275	Arg	Thr	Pro	Glu	Val	Thr 280	Cys	Val	Val	Val	Asp 285	Val	Ser	His
Glu 290	Asp	Pro	Glu	Val	Lys	Phe 295	Asn	Trp	Tyr	Val	Asp 300	Gly	Val	Glu	Val
His 305	Asn	Ala	Lys	Thr	Lys 310	Pro	Arg	Glu	Glu	Gln 315	Tyr	Asn	Ser	Thr	Tyr 320
Arg	Val	Val	Ser	Val 325	Leu	Thr	Val	Leu	His 330	Gln	Asp	Trp	Leu	Asn	Gly 335
Lys	Glu	Tyr	Lys 340	Cys	Lys	Val	Ser	Asn 345	Lys	Ala	Leu	Pro	Ala 350	Pro	Ile
Glu	Lys 355	Thr	Ile	Ser	Lys	Ala	Lys 360	Gly	Gln	Pro	Arg	Glu 365	Pro	Gln	Val
Tyr 370	Thr	Leu	Pro	Pro	Ser	Arg 375	Asp	Glu	Leu	Thr	Lys 380	Asn	Gln	Val	Ser
Leu 385	Thr	Cys	Leu	Val	Lys 390	Gly	Phe	Tyr	Pro	Ser 395	Asp	Ile	Ala	Val	Glu 400
Trp	Glu	Ser	Asn	Gly 405	Gln	Pro	Glu	Asn	Asn 410	Tyr	Lys	Thr	Thr	Pro 415	Pro
Val	Leu	Asp	Ser 420	Asp	Gly	Ser	Phe	Phe 425	Leu	Tyr	Ser	Lys	Leu 430	Thr	Val
Asp	Lys 435	Ser	Arg	Trp	Gln	Gln	Gly 440	Asn	Val	Phe	Ser	Cys 445	Ser	Val	Met

His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser
450						455					460				
Pro	Gly	Ser	Gly	Gly	Leu	Lys	Ile	Ala	Ala	Phe	Asn	Ile	Gln	Thr	Phe
465					470					475					480
Gly	Glu	Thr	Lys	Met	Ser	Asn	Ala	Thr	Leu	Val	Ser	Tyr	Ile	Val	Gln
				485					490					495	
Ile	Leu	Ser	Arg	Tyr	Asp	Ile	Ala	Leu	Val	Gln	Glu	Val	Arg	Asp	Ser
			500					505					510		
His	Leu	Thr	Ala	Val	Gly	Lys	Leu	Leu	Asp	Asn	Leu	Asn	Gln	Asp	Ala
		515					520					525			
Pro	Asp	Thr	Tyr	His	Tyr	Val	Val	Ser	Glu	Pro	Leu	Gly	Arg	Asn	Ser
	530					535					540				
Tyr	Lys	Glu	Arg	Tyr	Leu	Phe	Val	Tyr	Arg	Pro	Asp	Gln	Val	Ser	Ala
545					550					555					560
Val	Asp	Ser	Tyr	Tyr	Tyr	Asp	Asp	Gly	Cys	Glu	Pro	Cys	Gly	Asn	Asp
				565					570					575	
Thr	Phe	Asn	Arg	Glu	Pro	Ala	Ile	Val	Arg	Phe	Phe	Ser	Arg	Phe	Thr
			580					585					590		
Glu	Val	Arg	Glu	Phe	Ala	Ile	Val	Pro	Leu	His	Ala	Ala	Pro	Gly	Asp
		595					600					605			
Ala	Val	Ala	Glu	Ile	Asp	Ala	Leu	Tyr	Asp	Val	Tyr	Leu	Asp	Val	Gln
	610					615					620				
Glu	Lys	Trp	Gly	Leu	Glu	Asp	Val	Met	Leu	Met	Gly	Asp	Phe	Asn	Ala
625					630					635					640
Gly	Cys	Ser	Tyr	Val	Arg	Pro	Ser	Gln	Trp	Ser	Ser	Ile	Arg	Leu	Trp
				645					650					655	
Thr	Ser	Pro	Thr	Phe	Gln	Trp	Leu	Ile	Pro	Asp	Ser	Ala	Asp	Thr	Thr
			660					665					670		
Ala	Thr	Pro	Thr	His	Cys	Ala	Tyr	Asp	Arg	Ile	Val	Val	Ala	Gly	Met
		675					680					685			

Leu Leu Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn Phe
 690 695 700

Gln Ala Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp
 705 710 715 720

His Tyr Pro Val Glu Val Met Leu Lys
 725

<210> 53

<211> 2226

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 heavy chain - DNase I fusion

<400> 53

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gtgcagctgg tgcagtctgg ggcagaggtg aaaaagcctg gggcctcagt gaaggtgtcc	120
tgcaaggctt ctggctacac cttcagtgcc tactggatag agtgggtgcg ccaggctcca	180
ggaaagggcc tcgagtgggt cggagagatt ttacctggaa gtaataattc tagatacaat	240
gagaagttca agggccgagt gacagtcact agagacacat ccacaaacac agcctacatg	300
gagctcagca gcctgaggtc tgaggacaca gccgtctatt actgtgcaag atcctacgac	360
tttgccctggg ttgcttactg gggccaaggg actctgggtca cagtctcctc agcctccacc	420
aagggcccat cggctcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg	480
gccctgggct gcctgggtcaa ggactacttc cccgaaccgg tgacgggtgtc gtggaactca	540
ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac	600
tcctcagca gcgtgggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc	660
aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt	720
gacaaaactc acacatgccc accgtgcccga gcacctgaac tcctgggggg accgtcagtc	780
ttcctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca	840
tgcgtgggtgg tggacgtgag ccacgaagac cctgaggtca agttcaactg gtacgtggac	900
ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagtacaa cagcacgtac	960

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cgtgtggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag 1020
tgcaaggtct ccaacaaagc cctcccagcc cccatcgaga aaaccatctc caaagccaaa 1080
gggcagcccc gagaaccaca ggtgtacacc ctgcccccat cccgggatga gctgaccaag 1140
aaccaggtca gcctgacctg cctgggtcaaa ggcttctatc ccagcgacat cgccgtggag 1200
tgaggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc 1260
gacggctcct tcttcctcta cagcaagctc accgtggaca agagcagggtg gcagcagggg 1320
aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc 1380
ctctccctgt ctccgggtaa agggagcggc gggctgaaga tcgcagcctt caacatccag 1440
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agccgctacg acatcgccct ggtccaggag gtcagagaca gccacctgac tgccgtgggg 1560
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ccactgggac ggaacagcta taaggagcgc tacctgttcg tgtacaggcc tgaccagggtg 1680
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aaccgagagc cagccattgt caggttcttc tcccggttca cagaggtcag ggagtttgcc 1800
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aatgcgggct gcagctatgt gagaccctcc cagtggatcat ccatccgcct gtggacaagc 1980
cccaccttcc agtggctgat ccccgacagc gctgacacca cagctacacc cacgcactgt 2040
gcctatgaca ggatcgtggt tgcagggatg ctgctccgag gggccgttgt tcccgactcg 2100
gctcttccct ttaacttcca ggctgcctat ggctgagtg accaactggc ccaagccatc 2160
agtgaccact atccagtgga ggtgatgctg aagggggggcg gacccaaaaa gaagcgcaag 2220
gtttga 2226

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<210> 54

<211> 2226

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 heavy chain - DNase I fusion

<220>

<221> CDS

<222> (1)..(2226)

<223>

<400> 54

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Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly	
1 5 10 15	
gtc cac tcc cag gtg cag ctg gtg cag tct ggg gca gag gtg aaa aag	96
Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys	
20 25 30	
cct ggg gcc tca gtg aag gtg tcc tgc aag gct tct ggc tac acc ttc	144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe	
35 40 45	
agt gcc tac tgg ata gag tgg gtg cgc cag gct cca gga aag ggc ctc	192
Ser Ala Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu	
50 55 60	
gag tgg gtc gga gag att tta cct gga agt aat aat tct aga tac aat	240
Glu Trp Val Gly Glu Ile Leu Pro Gly Ser Asn Asn Ser Arg Tyr Asn	
65 70 75 80	
gag aag ttc aag ggc cga gtg aca gtc act aga gac aca tcc aca aac	288
Glu Lys Phe Lys Gly Arg Val Thr Val Thr Arg Asp Thr Ser Thr Asn	
85 90 95	
aca gcc tac atg gag ctc agc agc ctg agg tct gag gac aca gcc gtc	336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val	
100 105 110	
tat tac tgt gca aga tcc tac gac ttt gcc tgg ttt gct tac tgg ggc	384
Tyr Tyr Cys Ala Arg Ser Tyr Asp Phe Ala Trp Phe Ala Tyr Trp Gly	
115 120 125	
caa ggg act ctg gtc aca gtc tcc tca gcc tcc acc aag ggc cca tcg	432
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser	
130 135 140	
gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg	480
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala	
145 150 155 160	
gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg	528
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val	
165 170 175	
tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct	576
Ser Trp Asn Ser Gly Ala Leu Thr Ser Ser Gly Val His Thr Phe Pro Ala	
180 185 190	

gtc	cta	cag	tcc	tca	gga	ctc	tac	tcc	ctc	agc	agc	gtg	gtg	acc	gtg	624
Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	
		195					200					205				
ccc	tcc	agc	agc	ttg	ggc	acc	cag	acc	tac	atc	tgc	aac	gtg	aat	cac	672
Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	
	210					215					220					
aag	ccc	agc	aac	acc	aag	gtg	gac	aag	aaa	gtt	gag	ccc	aaa	tct	tgt	720
Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	
225					230					235					240	
gac	aaa	act	cac	aca	tgc	cca	ccg	tgc	cca	gca	cct	gaa	ctc	ctg	ggg	768
Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	
				245					250					255		
gga	ccg	tca	gtc	ttc	ctc	ttc	ccc	cca	aaa	ccc	aag	gac	acc	ctc	atg	816
Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	
			260					265					270			
atc	tcc	cgg	acc	cct	gag	gtc	aca	tgc	gtg	gtg	gtg	gac	gtg	agc	cac	864
Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	
		275					280					285				
gaa	gac	cct	gag	gtc	aag	ttc	aac	tgg	tac	gtg	gac	ggc	gtg	gag	gtg	912
Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	
	290					295					300					
cat	aat	gcc	aag	aca	aag	ccg	cgg	gag	gag	cag	tac	aac	agc	acg	tac	960
His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	
305					310					315					320	
cgt	gtg	gtc	agc	gtc	ctc	acc	gtc	ctg	cac	cag	gac	tgg	ctg	aat	ggc	1008
Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	
				325					330					335		
aag	gag	tac	aag	tgc	aag	gtc	tcc	aac	aaa	gcc	ctc	cca	gcc	ccc	atc	1056
Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	
			340					345					350			
gag	aaa	acc	atc	tcc	aaa	gcc	aaa	ggg	cag	ccc	cga	gaa	cca	cag	gtg	1104
Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	
		355					360					365				
tac	acc	ctg	ccc	cca	tcc	cgg	gat	gag	ctg	acc	aag	aac	cag	gtc	agc	1152
Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	
		370				375					380					
ctg	acc	tgc	ctg	gtc	aaa	ggc	ttc	tat	ccc	agc	gac	atc	gcc	gtg	gag	1200
Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	
385					390					395					400	
tgg	gag	agc	aat	ggg	cag	ccg	gag	aac	aac	tac	aag	acc	acg	cct	ccc	1248
Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	
				405					410					415		
gtg	ctg	gac	tcc	gac	ggc	tcc	ttc	ttc	ctc	tac	agc	aag	ctc	acc	gtg	1296
Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	

420	425	430	
gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met 435 440 445			1344
cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg tct His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser 450 455 460			1392
ccg ggt aaa ggg agc ggc ggg ctg aag atc gca gcc ttc aac atc cag Pro Gly Lys Gly Ser Gly Gly Leu Lys Ile Ala Ala Phe Asn Ile Gln 465 470 475 480			1440
aca ttt ggg gag acc aag atg tcc aat gcc acc ctc gtc agc tac att Thr Phe Gly Glu Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile 485 490 495			1488
gtg cag atc ctg agc cgc tac gac atc gcc ctg gtc cag gag gtc aga Val Gln Ile Leu Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg 500 505 510			1536
gac agc cac ctg act gcc gtg ggg aag ctg ctg gac aac ctc aat cag Asp Ser His Leu Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln 515 520 525			1584
gac gca cca gac acc tat cac tac gtg gtc agt gag cca ctg gga cgg Asp Ala Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg 530 535 540			1632
aac agc tat aag gag cgc tac ctg ttc gtg tac agg cct gac cag gtg Asn Ser Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val 545 550 555 560			1680
tct gcg gtg gac agc tac tac tac gat gat ggc tgc gag ccc tgc ggg Ser Ala Val Asp Ser Tyr Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly 565 570 575			1728
aac gac acc ttc aac cga gag cca gcc att gtc agg ttc ttc tcc cgg Asn Asp Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg 580 585 590			1776
ttc aca gag gtc agg gag ttt gcc att gtt ccc ctg cat gcg gcc ccg Phe Thr Glu Val Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro 595 600 605			1824
ggg gac gca gta gcc gag atc gac gct ctc tat gac gtc tac ctg gat Gly Asp Ala Val Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp 610 615 620			1872
gtc caa gag aaa tgg ggc ttg gag gac gtc atg ttg atg ggc gac ttc Val Gln Glu Lys Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe 625 630 635 640			1920
aat gcg ggc tgc agc tat gtg aga ccc tcc cag tgg tca tcc atc cgc Asn Ala Gly Cys Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg 645 650 655			1968
ctg tgg aca agc ccc acc ttc cag tgg ctg atc ccc gac agc gct gac			2016

Leu	Trp	Thr	Ser	Pro	Thr	Phe	Gln	Trp	Leu	Ile	Pro	Asp	Ser	Ala	Asp	
			660					665					670			
acc	aca	gct	aca	ccc	acg	cac	tgt	gcc	tat	gac	agg	atc	gtg	ggt	gca	2064
Thr	Thr	Ala	Thr	Pro	Thr	His	Cys	Ala	Tyr	Asp	Arg	Ile	Val	Val	Ala	
		675					680					685				
ggg	atg	ctg	ctc	cga	ggg	gcc	gtt	gtt	ccc	gac	tcg	gct	ctt	ccc	ttt	2112
Gly	Met	Leu	Leu	Arg	Gly	Ala	Val	Val	Pro	Asp	Ser	Ala	Leu	Pro	Phe	
	690					695					700					
aac	ttc	cag	gct	gcc	tat	ggc	ctg	agt	gac	caa	ctg	gcc	caa	gcc	atc	2160
Asn	Phe	Gln	Ala	Ala	Tyr	Gly	Leu	Ser	Asp	Gln	Leu	Ala	Gln	Ala	Ile	
705					710				715						720	
agt	gac	cac	tat	cca	gtg	gag	gtg	atg	ctg	aag	ggg	ggc	gga	ccc	aaa	2208
Ser	Asp	His	Tyr	Pro	Val	Glu	Val	Met	Leu	Lys	Gly	Gly	Gly	Pro	Lys	
				725					730					735		
aag	aag	cgc	aag	ggt	tga											2226
Lys	Lys	Arg	Lys	Val												
			740													

<210> 55

<211> 741

<212> PRT

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 heavy chain - DNase I fusion

<400> 55

Met	Gly	Trp	Ser	Cys	Ile	Ile	Leu	Phe	Leu	Val	Ala	Thr	Ala	Thr	Gly	
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Val	His	Ser	Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	
			20					25					30			
Pro	Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	
		35					40					45				
Ser	Ala	Tyr	Trp	Ile	Glu	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	
	50					55					60					
Glu	Trp	Val	Gly	Glu	Ile	Leu	Pro	Gly	Ser	Asn	Asn	Ser	Arg	Tyr	Asn	
65					70					75					80	

Glu	Lys	Phe	Lys	Gly	Arg	Val	Thr	Val	Thr	Arg	Asp	Thr	Ser	Thr	Asn
				85					90					95	
Thr	Ala	Tyr	Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val
			100					105					110		
Tyr	Tyr	Cys	Ala	Arg	Ser	Tyr	Asp	Phe	Ala	Trp	Phe	Ala	Tyr	Trp	Gly
		115					120					125			
Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser
	130					135					140				
Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala
145					150					155					160
Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val
				165					170					175	
Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala
			180					185					190		
Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val
		195					200					205			
Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His
	210					215					220				
Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys
225					230					235					240
Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly
				245					250					255	
Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met
			260					265					270		
Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His
		275					280					285			
Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val
	290					295					300				
His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr
305					310					315					320

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
 325 330 335
 Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
 340 345 350
 Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
 355 360 365
 Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
 370 375 380
 Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
 385 390 395 400
 Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
 405 410 415
 Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
 420 425 430
 Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
 435 440 445
 His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
 450 455 460
 Pro Gly Lys Gly Ser Gly Gly Leu Lys Ile Ala Ala Phe Asn Ile Gln
 465 470 475 480
 Thr Phe Gly Glu Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile
 485 490 495
 Val Gln Ile Leu Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg
 500 505 510
 Asp Ser His Leu Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln
 515 520 525
 Asp Ala Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg
 530 535 540
 Asn Ser Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val

545 550 555 560

Ser Ala Val Asp Ser Tyr Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly
565 570 575

Asn Asp Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg
580 585 590

Phe Thr Glu Val Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro
595 600 605

Gly Asp Ala Val Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp
610 615 620

Val Gln Glu Lys Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe
625 630 635 640

Asn Ala Gly Cys Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg
645 650 655

Leu Trp Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp
660 665 670

Thr Thr Ala Thr Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala
675 680 685

Gly Met Leu Leu Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe
690 695 700

Asn Phe Gln Ala Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile
705 710 715 720

Ser Asp His Tyr Pro Val Glu Val Met Leu Lys Gly Gly Gly Pro Lys
725 730 735

Lys Lys Arg Lys Val
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<210> 56

<211> 2223

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 heavy chain - DNase I fusion

<400> 56

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tgcaaggctt ctggctacac cttcagtgcc tactggatag agtgggtgcg ccaggctcca	180
ggaaagggcc tcgagtgggt cggagagatt ttacctggaa gtaataattc tagatacaat	240
gagaagttca agggccgagt gacagtcact agagacacat ccacaaacac agcctacatg	300
gagctcagca gcctgaggtc tgaggacaca gccgtctatt actgtgcaag atcctacgac	360
tttgcctggg ttgcttactg gggccaaggg actctgggtca cagtctcctc agcctccacc	420
aagggcccat cggctcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg	480
gccttggggt gcctgggtcaa ggactacttc cccgaaccgg tgacgggtgtc gtggaactca	540
ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac	600
tcctcagca gcgtgggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc	660
aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt	720
gacaaaactc acacatgccc accgtgcca gcacctgaac tcctgggggg accgtcagtc	780
ttcctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca	840
tgcgtgggtg tggacgtgag ccacgaagac cctgaggtca agttcaactg gtacgtggac	900
ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagtacaa cagcacgtac	960
cgtgtgggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag	1020
tgcaagggtct ccaacaaagc cctcccagcc cccatcgaga aaaccatctc caaagccaaa	1080
gggcagcccc gagaaccaca ggtgtacacc ctgcccccat ccgggatga gctgaccaag	1140
aaccaggtca gcctgacctg cctgggtcaaa ggcttctatc ccagcgacat cgccgtggag	1200
tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc	1260
gacggctcct tcttctctta cagcaagctc accgtggaca agagcaggtg gcagcagggg	1320
aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc	1380
ctctccctgt ctccgaaggg gagcggcggg ctgaagatcg cagccttcaa catccagaca	1440
tttggggaga ccaagatgtc caatgccacc ctcgtcagct acattgtgca gatcctgagc	1500
cgctacgaca tcgccctggg ccaggaggtc agagacagcc acctgactgc cgtggggaag	1560

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ctgctggaca acctcaatca ggacgcacca gacacctatc actacgtggt cagtgaacca 1620
ctgggacgga acagctataa ggagcgctac ctgttcgtgt acaggcctga ccaggtgtct 1680
gcggtggaca gctactacta cgatgatggc tgcgagccct gcgggaacga caccttcaac 1740
cgagagccag ccattgtcag gttcttctcc cggttcacag aggtcaggga gtttgccatt 1800
gttcccctgc atgcggcccc gggggacgca gtagccgaga tcgacgtctt ctatgacgtc 1860
tacctggatg tccaagagaa atggggcttg gaggacgtca tggtgatggg cgacttcaat 1920
gcgggctgca gctatgtgag accctcccag tggatcatcca tccgctgtg gacaagcccc 1980
accttccagt ggctgatccc cgacagcgct gacaccacag ctacacccac gcactgtgcc 2040
tatgacagga tcgtgggtgc agggatgctg ctccgagggg ccgttggtcc cgactcggct 2100
cttcccttta acttccaggc tgcctatggc ctgagtgacc aactggcca agccatcagt 2160
gaccactatc cagtggaggt gatgctgaag gggggcggac ccaaaaagaa gcgcaagggt 2220
tga 2223

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<210> 57

<211> 2223

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 heavy chain - DNase I fusion

<220>

<221> CDS

<222> (1)..(2223)

<223>

<400> 57

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Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1 5 10 15

gtc cac tcc cag gtg cag ctg gtg cag tct ggg gca gag gtg aaa aag 96
Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

cct ggg gcc tca gtg aag gtg tcc tgc aag gct tct ggc tac acc ttc 144

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Pro	Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	
		35					40					45				
agt	gcc	tac	tgg	ata	gag	tgg	gtg	cgc	cag	gct	cca	gga	aag	ggc	ctc	192
Ser	Ala	Tyr	Trp	Ile	Glu	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	
	50					55					60					
gag	tgg	gtc	gga	gag	att	tta	cct	gga	agt	aat	aat	tct	aga	tac	aat	240
Glu	Trp	Val	Gly	Glu	Ile	Leu	Pro	Gly	Ser	Asn	Asn	Ser	Arg	Tyr	Asn	
65					70					75					80	
gag	aag	ttc	aag	ggc	cga	gtg	aca	gtc	act	aga	gac	aca	tcc	aca	aac	288
Glu	Lys	Phe	Lys	Gly	Arg	Val	Thr	Val	Thr	Arg	Asp	Thr	Ser	Thr	Asn	
				85					90					95		
aca	gcc	tac	atg	gag	ctc	agc	agc	ctg	agg	tct	gag	gac	aca	gcc	gtc	336
Thr	Ala	Tyr	Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	
			100					105					110			
tat	tac	tgt	gca	aga	tcc	tac	gac	ttt	gcc	tgg	ttt	gct	tac	tgg	ggc	384
Tyr	Tyr	Cys	Ala	Arg	Ser	Tyr	Asp	Phe	Ala	Trp	Phe	Ala	Tyr	Trp	Gly	
		115					120					125				
caa	ggg	act	ctg	gtc	aca	gtc	tcc	tca	gcc	tcc	acc	aag	ggc	cca	tcg	432
Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	
	130					135					140					
gtc	ttc	ccc	ctg	gca	ccc	tcc	tcc	aag	agc	acc	tct	ggg	ggc	aca	gcg	480
Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	
145					150					155					160	
gcc	ctg	ggc	tgc	ctg	gtc	aag	gac	tac	ttc	ccc	gaa	ccg	gtg	acg	gtg	528
Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	
				165					170					175		
tcg	tgg	aac	tca	ggc	gcc	ctg	acc	agc	ggc	gtg	cac	acc	ttc	ccg	gct	576
Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	
			180					185					190			
gtc	cta	cag	tcc	tca	gga	ctc	tac	tcc	ctc	agc	agc	gtg	gtg	acc	gtg	624
Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	
		195					200					205				
ccc	tcc	agc	agc	ttg	ggc	acc	cag	acc	tac	atc	tgc	aac	gtg	aat	cac	672
Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	
	210					215					220					
aag	ccc	agc	aac	acc	aag	gtg	gac	aag	aaa	gtt	gag	ccc	aaa	tct	tgt	720
Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	
225					230					235					240	
gac	aaa	act	cac	aca	tgc	cca	ccg	tgc	cca	gca	cct	gaa	ctc	ctg	ggg	768
Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	
				245					250					255		
gga	ccg	tca	gtc	ttc	ctc	ttc	ccc	cca	aaa	ccc	aag	gac	acc	ctc	atg	816
Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	
			260					265						270		

atc	tcc	cgg	acc	cct	gag	gtc	aca	tgc	gtg	gtg	gtg	gac	gtg	agc	cac	864
Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	
		275					280					285				
gaa	gac	cct	gag	gtc	aag	ttc	aac	tgg	tac	gtg	gac	ggc	gtg	gag	gtg	912
Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	
		290				295					300					
cat	aat	gcc	aag	aca	aag	ccg	cgg	gag	gag	cag	tac	aac	agc	acg	tac	960
His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	
305					310					315					320	
cgt	gtg	gtc	agc	gtc	ctc	acc	gtc	ctg	cac	cag	gac	tgg	ctg	aat	ggc	1008
Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	
				325					330					335		
aag	gag	tac	aag	tgc	aag	gtc	tcc	aac	aaa	gcc	ctc	cca	gcc	ccc	atc	1056
Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	
			340					345					350			
gag	aaa	acc	atc	tcc	aaa	gcc	aaa	ggg	cag	ccc	cga	gaa	cca	cag	gtg	1104
Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	
		355					360					365				
tac	acc	ctg	ccc	cca	tcc	cgg	gat	gag	ctg	acc	aag	aac	cag	gtc	agc	1152
Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	
		370				375					380					
ctg	acc	tgc	ctg	gtc	aaa	ggc	ttc	tat	ccc	agc	gac	atc	gcc	gtg	gag	1200
Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	
385					390					395					400	
tgg	gag	agc	aat	ggg	cag	ccg	gag	aac	aac	tac	aag	acc	acg	cct	ccc	1248
Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	
				405				410						415		
gtg	ctg	gac	tcc	gac	ggc	tcc	ttc	ttc	ctc	tac	agc	aag	ctc	acc	gtg	1296
Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	
			420				425						430			
gac	aag	agc	agg	tgg	cag	cag	ggg	aac	gtc	ttc	tca	tgc	tcc	gtg	atg	1344
Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	
		435					440					445				
cat	gag	gct	ctg	cac	aac	cac	tac	acg	cag	aag	agc	ctc	tcc	ctg	tct	1392
His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	
		450				455					460					
ccg	aag	ggg	agc	ggc	ggg	ctg	aag	atc	gca	gcc	ttc	aac	atc	cag	aca	1440
Pro	Lys	Gly	Ser	Gly	Gly	Leu	Lys	Ile	Ala	Ala	Phe	Asn	Ile	Gln	Thr	
465					470					475					480	
ttt	ggg	gag	acc	aag	atg	tcc	aat	gcc	acc	ctc	gtc	agc	tac	att	gtg	1488
Phe	Gly	Glu	Thr	Lys	Met	Ser	Asn	Ala	Thr	Leu	Val	Ser	Tyr	Ile	Val	
				485				490						495		
cag	atc	ctg	agc	cgc	tac	gac	atc	gcc	ctg	gtc	cag	gag	gtc	aga	gac	1536
Gln	Ile	Leu	Ser	Arg	Tyr	Asp	Ile	Ala	Leu	Val	Gln	Glu	Val	Arg	Asp	
			500					505					510			

[illegible]

740

<210> 58

<211> 740

<212> PRT

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 heavy chain - DNase I fusion

<400> 58

Met	Gly	Trp	Ser	Cys	Ile	Ile	Leu	Phe	Leu	Val	Ala	Thr	Ala	Thr	Gly
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Val	His	Ser	Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys
			20					25					30		

Pro	Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe
		35					40					45			

Ser	Ala	Tyr	Trp	Ile	Glu	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu
	50					55					60				

Glu	Trp	Val	Gly	Glu	Ile	Leu	Pro	Gly	Ser	Asn	Asn	Ser	Arg	Tyr	Asn
65					70					75					80

Glu	Lys	Phe	Lys	Gly	Arg	Val	Thr	Val	Thr	Arg	Asp	Thr	Ser	Thr	Asn
				85					90					95	

Thr	Ala	Tyr	Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val
			100					105					110		

Tyr	Tyr	Cys	Ala	Arg	Ser	Tyr	Asp	Phe	Ala	Trp	Phe	Ala	Tyr	Trp	Gly
		115					120					125			

Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser
	130					135					140				

Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala
145					150					155					160

Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	165	170	175
Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	180	185	190
Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	195	200	205
Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	210	215	220
Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	225	230	235
Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	245	250	255
Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	260	265	270
Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	275	280	285
Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	290	295	300
His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	305	310	315
Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	325	330	335
Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	340	345	350
Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	355	360	365
Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	370	375	380
Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	385	390	395
																		400

Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	405	410	415	
Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	420	425	430	
Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	435	440	445	
His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	450	455	460	
Pro	Lys	Gly	Ser	Gly	Gly	Leu	Lys	Ile	Ala	Ala	Phe	Asn	Ile	Gln	Thr	465	470	475	480
Phe	Gly	Glu	Thr	Lys	Met	Ser	Asn	Ala	Thr	Leu	Val	Ser	Tyr	Ile	Val	485	490	495	
Gln	Ile	Leu	Ser	Arg	Tyr	Asp	Ile	Ala	Leu	Val	Gln	Glu	Val	Arg	Asp	500	505	510	
Ser	His	Leu	Thr	Ala	Val	Gly	Lys	Leu	Leu	Asp	Asn	Leu	Asn	Gln	Asp	515	520	525	
Ala	Pro	Asp	Thr	Tyr	His	Tyr	Val	Val	Ser	Glu	Pro	Leu	Gly	Arg	Asn	530	535	540	
Ser	Tyr	Lys	Glu	Arg	Tyr	Leu	Phe	Val	Tyr	Arg	Pro	Asp	Gln	Val	Ser	545	550	555	560
Ala	Val	Asp	Ser	Tyr	Tyr	Tyr	Asp	Asp	Gly	Cys	Glu	Pro	Cys	Gly	Asn	565	570	575	
Asp	Thr	Phe	Asn	Arg	Glu	Pro	Ala	Ile	Val	Arg	Phe	Phe	Ser	Arg	Phe	580	585	590	
Thr	Glu	Val	Arg	Glu	Phe	Ala	Ile	Val	Pro	Leu	His	Ala	Ala	Pro	Gly	595	600	605	
Asp	Ala	Val	Ala	Glu	Ile	Asp	Ala	Leu	Tyr	Asp	Val	Tyr	Leu	Asp	Val	610	615	620	
Gln	Glu	Lys	Trp	Gly	Leu	Glu	Asp	Val	Met	Leu	Met	Gly	Asp	Phe	Asn	625	630	635	640

Ala Gly Cys Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu
645 650 655

Trp Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr
660 665 670

Thr Ala Thr Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly
675 680 685

Met Leu Leu Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn
690 695 700

Phe Gln Ala Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser
705 710 715 720

Asp His Tyr Pro Val Glu Val Met Leu Lys Gly Gly Gly Pro Lys Lys
725 730 735

Lys Arg Lys Val
740

<210> 59

<211> 2220

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 heavy chain - DNase I fusion

<400> 59

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gtgcagctgg tgcagtctgg ggcagaggtg aaaaagcctg ggcctcagt gaaggtgtcc	120
tgcaaggctt ctggctacac cttcagtgcc tactggatag agtgggtgcg ccaggctcca	180
ggaaagggcc tcgagtgggt cggagagatt ttacctggaa gtaataattc tagatacaat	240
gagaagttca agggccgagt gacagtcact agagacacat ccacaaacac agcctacatg	300
gagctcagca gcctgaggtc tgaggacaca gccgtctatt actgtgcaag atcctacgac	360
tttgcttggt ttgcttactg gggccaaggg actctggtca cagtctcctc agcctccacc	420

aagggcccat	cggtcttccc	cctggcaccc	tcctccaaga	gcacctctgg	gggcacagcg	480
gccctgggct	gcctgggtcaa	ggactacttc	cccgaaccgg	tgacgggtgtc	gtggaactca	540
ggcgccctga	ccagcggcgt	gcacaccttc	ccggctgtcc	tacagtcctc	aggactctac	600
tcctcagca	gcgtgggtgac	cgtgccctcc	agcagcttgg	gcaccagac	ctacatctgc	660
aacgtgaatc	acaagcccag	caacaccaag	gtggacaaga	aagttgagcc	caaatcttgt	720
gacaaaactc	acacatgccc	accgtgccc	gcacctgaac	tcctgggggg	accgtcagtc	780
ttcctcttcc	ccccaaaacc	caaggacacc	ctcatgatct	cccggacccc	tgaggtcaca	840
tgcggtgggtg	tggacgtgag	ccacgaagac	cctgaggtca	agttcaactg	gtacgtggac	900
ggcggtggagg	tgcataatgc	caagacaaag	ccgcgggagg	agcagtacaa	cagcacgtac	960
cgtgtgggtca	gcgtcctcac	cgtcctgcac	caggactggc	tgaatggcaa	ggagtacaag	1020
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gggcagcccc	gagaaccaca	ggtgtacacc	ctgcccccat	cccgggatga	gctgaccaag	1140
aaccaggtca	gcctgacctg	cctgggtcaaa	ggcttctatc	ccagcgacat	cgccgtggag	1200
tgggagagca	atgggcagcc	ggagaacaac	tacaagacca	cgcctcccg	gctggactcc	1260
gacggctcct	tcttcctcta	cagcaagctc	accgtggaca	agagcaggtg	gcagcagggg	1320
aacgtcttct	catgctccgt	gatgcatgag	gctctgcaca	accactacac	gcagaagagc	1380
ctctccctgt	ccccggggag	cggcgggctg	aagatcgag	ccttcaacat	ccagacattt	1440
ggggagacca	agatgtccaa	tgccaccctc	gtcagctaca	ttgtgcagat	cctgagccgc	1500
tacgacatcg	ccctgggtcca	ggaggtcaga	gacagccacc	tgactgccgt	ggggaagctg	1560
ctggacaacc	tcaatcagga	cgcaccagac	acctatcact	acgtggtcag	tgagccactg	1620
ggacggaaca	gctataagga	gcgctacctg	ttcgtgtaca	ggcctgacca	ggtgtctgcg	1680
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gagccagcca	ttgtcaggtt	cttctcccgg	ttcacagagg	tcaggaggtt	tgccattggt	1800
ccctgcatg	cggccccggg	ggacgcagta	gccgagatcg	acgctctcta	tgacgtctac	1860
ctggatgtcc	aagagaaatg	gggcttggag	gacgtcatgt	tgatgggcga	cttcaatgcg	1920
ggctgcagct	atgtgagacc	ctcccagtgg	tcattccatcc	gcctgtggac	aagccccacc	1980
ttccagtggc	tgatccccga	cagcgtgac	accacagcta	caccacgca	ctgtgcctat	2040
gacaggatcg	tggttgcagg	gatgctgctc	cgaggggccg	ttgttcccga	ctcggctctt	2100
ccctttaact	tccaggctgc	ctatggcctg	agtgaccaac	tggcccaagc	catcagtgac	2160
cactatccag	tggaggtgat	gctgaagggg	ggcggaccca	aaaagaagcg	caaggtttga	2220

<210> 60

<211> 2220

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 heavy chain - DNase I fusion

<220>

<221> CDS

<222> (1)..(2220)

<223>

<400> 60

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Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly	
1 5 10 15	
gtc cac tcc cag gtg cag ctg gtg cag tct ggg gca gag gtg aaa aag	96
Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys	
20 25 30	
cct ggg gcc tca gtg aag gtg tcc tgc aag gct tct ggc tac acc ttc	144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe	
35 40 45	
agt gcc tac tgg ata gag tgg gtg cgc cag gct cca gga aag ggc ctc	192
Ser Ala Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu	
50 55 60	
gag tgg gtc gga gag att tta cct gga agt aat aat tct aga tac aat	240
Glu Trp Val Gly Glu Ile Leu Pro Gly Ser Asn Asn Ser Arg Tyr Asn	
65 70 75 80	
gag aag ttc aag ggc cga gtg aca gtc act aga gac aca tcc aca aac	288
Glu Lys Phe Lys Gly Arg Val Thr Val Thr Arg Asp Thr Ser Thr Asn	
85 90 95	
aca gcc tac atg gag ctc agc agc ctg agg tct gag gac aca gcc gtc	336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val	
100 105 110	
tat tac tgt gca aga tcc tac gac ttt gcc tgg ttt gct tac tgg ggc	384
Tyr Tyr Cys Ala Arg Ser Tyr Asp Phe Ala Trp Phe Ala Tyr Trp Gly	
115 120 125	

caa	ggg	act	ctg	gtc	aca	gtc	tcc	tca	gcc	tcc	acc	aag	ggc	cca	tcg	432
Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	
	130					135					140					
gtc	ttc	ccc	ctg	gca	ccc	tcc	tcc	aag	agc	acc	tct	ggg	ggc	aca	gcg	480
Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	
145					150					155					160	
gcc	ctg	ggc	tgc	ctg	gtc	aag	gac	tac	ttc	ccc	gaa	ccg	gtg	acg	gtg	528
Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	
				165					170					175		
tcg	tgg	aac	tca	ggc	gcc	ctg	acc	agc	ggc	gtg	cac	acc	ttc	ccg	gct	576
Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	
			180					185					190			
gtc	cta	cag	tcc	tca	gga	ctc	tac	tcc	ctc	agc	agc	gtg	gtg	acc	gtg	624
Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	
		195					200					205				
ccc	tcc	agc	agc	ttg	ggc	acc	cag	acc	tac	atc	tgc	aac	gtg	aat	cac	672
Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	
	210					215					220					
aag	ccc	agc	aac	acc	aag	gtg	gac	aag	aaa	gtt	gag	ccc	aaa	tct	tgt	720
Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	
225					230					235					240	
gac	aaa	act	cac	aca	tgc	cca	ccg	tgc	cca	gca	cct	gaa	ctc	ctg	ggg	768
Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	
				245					250					255		
gga	ccg	tca	gtc	ttc	ctc	ttc	ccc	cca	aaa	ccc	aag	gac	acc	ctc	atg	816
Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	
			260				265						270			
atc	tcc	cgg	acc	cct	gag	gtc	aca	tgc	gtg	gtg	gtg	gac	gtg	agc	cac	864
Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	
		275					280					285				
gaa	gac	cct	gag	gtc	aag	ttc	aac	tgg	tac	gtg	gac	ggc	gtg	gag	gtg	912
Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	
	290					295					300					
cat	aat	gcc	aag	aca	aag	ccg	cgg	gag	gag	cag	tac	aac	agc	acg	tac	960
His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	
305					310					315					320	
cgt	gtg	gtc	agc	gtc	ctc	acc	gtc	ctg	cac	cag	gac	tgg	ctg	aat	ggc	1008
Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	
				325					330					335		
aag	gag	tac	aag	tgc	aag	gtc	tcc	aac	aaa	gcc	ctc	cca	gcc	ccc	atc	1056
Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	
			340					345					350			
gag	aaa	acc	atc	tcc	aaa	gcc	aaa	ggg	cag	ccc	cga	gaa	cca	cag	gtg	1104
Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	
		355				360						365				

tac	acc	ctg	ccc	cca	tcc	cgg	gat	gag	ctg	acc	aag	aac	cag	gtc	agc	1152
Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	
	370					375					380					
ctg	acc	tgc	ctg	gtc	aaa	ggc	ttc	tat	ccc	agc	gac	atc	gcc	gtg	gag	1200
Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	
385					390					395					400	
tgg	gag	agc	aat	ggg	cag	ccg	gag	aac	aac	tac	aag	acc	acg	cct	ccc	1248
Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	
				405					410					415		
gtg	ctg	gac	tcc	gac	ggc	tcc	ttc	ttc	ctc	tac	agc	aag	ctc	acc	gtg	1296
Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	
			420					425					430			
gac	aag	agc	agg	tgg	cag	cag	ggg	aac	gtc	ttc	tca	tgc	tcc	gtg	atg	1344
Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	
		435					440					445				
cat	gag	gct	ctg	cac	aac	cac	tac	acg	cag	aag	agc	ctc	tcc	ctg	tcc	1392
His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	
	450					455					460					
ccg	ggg	agc	ggc	ggg	ctg	aag	atc	gca	gcc	ttc	aac	atc	cag	aca	ttt	1440
Pro	Gly	Ser	Gly	Gly	Leu	Lys	Ile	Ala	Ala	Phe	Asn	Ile	Gln	Thr	Phe	
465					470					475					480	
ggg	gag	acc	aag	atg	tcc	aat	gcc	acc	ctc	gtc	agc	tac	att	gtg	cag	1488
Gly	Glu	Thr	Lys	Met	Ser	Asn	Ala	Thr	Leu	Val	Ser	Tyr	Ile	Val	Gln	
				485					490					495		
atc	ctg	agc	cgc	tac	gac	atc	gcc	ctg	gtc	cag	gag	gtc	aga	gac	agc	1536
Ile	Leu	Ser	Arg	Tyr	Asp	Ile	Ala	Leu	Val	Gln	Glu	Val	Arg	Asp	Ser	
			500					505					510			
cac	ctg	act	gcc	gtg	ggg	aag	ctg	ctg	gac	aac	ctc	aat	cag	gac	gca	1584
His	Leu	Thr	Ala	Val	Gly	Lys	Leu	Leu	Asp	Asn	Leu	Asn	Gln	Asp	Ala	
		515					520					525				
cca	gac	acc	tat	cac	tac	gtg	gtc	agt	gag	cca	ctg	gga	cgg	aac	agc	1632
Pro	Asp	Thr	Tyr	His	Tyr	Val	Val	Ser	Glu	Pro	Leu	Gly	Arg	Asn	Ser	
	530					535					540					
tat	aag	gag	cgc	tac	ctg	ttc	gtg	tac	agg	cct	gac	cag	gtg	tct	gcg	1680
Tyr	Lys	Glu	Arg	Tyr	Leu	Phe	Val	Tyr	Arg	Pro	Asp	Gln	Val	Ser	Ala	
545					550					555					560	
gtg	gac	agc	tac	tac	tac	gat	gat	ggc	tgc	gag	ccc	tgc	ggg	aac	gac	1728
Val	Asp	Ser	Tyr	Tyr	Tyr	Asp	Asp	Gly	Cys	Glu	Pro	Cys	Gly	Asn	Asp	
				565					570					575		
acc	ttc	aac	cga	gag	cca	gcc	att	gtc	agg	ttc	ttc	tcc	cgg	ttc	aca	1776
Thr	Phe	Asn	Arg	Glu	Pro	Ala	Ile	Val	Arg	Phe	Phe	Ser	Arg	Phe	Thr	
			580					585					590			
gag	gtc	agg	gag	ttt	gcc	att	gtt	ccc	ctg	cat	gcg	gcc	ccg	ggg	gac	1824
Glu	Val	Arg	Glu	Phe	Ala	Ile	Val	Pro	Leu	His	Ala	Ala	Pro	Gly	Asp	

595	600	605	
gca gta gcc gag atc gac gct ctc tat gac gtc tac ctg gat gtc caa Ala Val Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val Gln 610 615 620			1872
gag aaa tgg ggc ttg gag gac gtc atg ttg atg ggc gac ttc aat gcg Glu Lys Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn Ala 625 630 635 640			1920
ggc tgc agc tat gtg aga ccc tcc cag tgg tca tcc atc cgc ctg tgg Gly Cys Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu Trp 645 650 655			1968
aca agc ccc acc ttc cag tgg ctg atc ccc gac agc gct gac acc aca Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr Thr 660 665 670			2016
gct aca ccc acg cac tgt gcc tat gac agg atc gtg gtt gca ggg atg Ala Thr Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly Met 675 680 685			2064
ctg ctc cga ggg gcc gtt gtt ccc gac tcg gct ctt ccc ttt aac ttc Leu Leu Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn Phe 690 695 700			2112
cag gct gcc tat ggc ctg agt gac caa ctg gcc caa gcc atc agt gac Gln Ala Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp 705 710 715 720			2160
cac tat cca gtg gag gtg atg ctg aag ggg ggc gga ccc aaa aag aag His Tyr Pro Val Glu Val Met Leu Lys Gly Gly Gly Pro Lys Lys Lys 725 730 735			2208
cgc aag gtt tga Arg Lys Val			2220

<210> 61

<211> 739

<212> PRT

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 heavy chain - DNase I fusion

<400> 61

Met	Gly	Trp	Ser	Cys	Ile	Ile	Leu	Phe	Leu	Val	Ala	Thr	Ala	Thr	Gly
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Val	His	Ser	Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	20	25	30	
Pro	Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	35	40	45	
Ser	Ala	Tyr	Trp	Ile	Glu	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	50	55	60	
Glu	Trp	Val	Gly	Glu	Ile	Leu	Pro	Gly	Ser	Asn	Asn	Ser	Arg	Tyr	Asn	65	70	75	80
Glu	Lys	Phe	Lys	Gly	Arg	Val	Thr	Val	Thr	Arg	Asp	Thr	Ser	Thr	Asn	85	90	95	
Thr	Ala	Tyr	Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	100	105	110	
Tyr	Tyr	Cys	Ala	Arg	Ser	Tyr	Asp	Phe	Ala	Trp	Phe	Ala	Tyr	Trp	Gly	115	120	125	
Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	130	135	140	
Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	145	150	155	160
Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	165	170	175	
Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	180	185	190	
Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	195	200	205	
Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	210	215	220	
Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	225	230	235	240
Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	245	250	255	

Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met
			260					265					270		
Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His
		275					280					285			
Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val
	290					295					300				
His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr
305					310					315					320
Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly
				325					330					335	
Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile
			340					345					350		
Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val
		355					360					365			
Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser
	370					375					380				
Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu
385					390					395					400
Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro
				405					410					415	
Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val
			420					425					430		
Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met
		435					440					445			
His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser
	450					455					460				
Pro	Gly	Ser	Gly	Gly	Leu	Lys	Ile	Ala	Ala	Phe	Asn	Ile	Gln	Thr	Phe
465					470					475					480
Gly	Glu	Thr	Lys	Met	Ser	Asn	Ala	Thr	Leu	Val	Ser	Tyr	Ile	Val	Gln
				485					490					495	

Ile Leu Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp Ser
500 505 510

His Leu Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp Ala
515 520 525

Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn Ser
530 535 540

Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser Ala
545 550 555 560

Val Asp Ser Tyr Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn Asp
565 570 575

Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe Thr
580 585 590

Glu Val Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly Asp
595 600 605

Ala Val Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val Gln
610 615 620

Glu Lys Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn Ala
625 630 635 640

Gly Cys Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu Trp
645 650 655

Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr Thr
660 665 670

Ala Thr Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly Met
675 680 685

Leu Leu Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn Phe
690 695 700

Gln Ala Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp
705 710 715 720

His Tyr Pro Val Glu Val Met Leu Lys Gly Gly Gly Pro Lys Lys Lys

725

730

735

Arg Lys Val

<210> 62

<211> 1548

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 62

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<210> 63

<211> 1548

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 63

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<210> 64

<211> 1557

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 64

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<210> 65

<211> 1548

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<220>

<221> CDS

<222> (1) .. (1548)

<223>

<400> 65

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Val	His	Ser	Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	
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cct	ggg	gcc	tca	gtg	aag	gtg	tcc	tgc	aag	gct	tct	ggc	tac	acc	ttc	144
Pro	Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	
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Ser	Ala	Tyr	Trp	Ile	Glu	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	
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Glu	Trp	Val	Gly	Glu	Ile	Leu	Pro	Gly	Ser	Asn	Asn	Ser	Arg	Tyr	Asn	
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Glu	Lys	Phe	Lys	Gly	Arg	Val	Thr	Val	Thr	Arg	Asp	Thr	Ser	Thr	Asn	
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Thr	Ala	Tyr	Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	
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Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	
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Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	
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Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	
		195					200					205				
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Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	
	210					215					220					
aag	ccc	agc	aac	acc	aag	gtg	gac	aag	aaa	gtt	gag	ccc	aaa	tct	tgt	720
Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	
225					230					235					240	

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Val Pro Asp Ser Ala Leu Pro Phe Asn Phe Gln Ala Ala Tyr Gly Leu							
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agt gac caa ctg gcc caa gcc atc agt gac cac tat cca gtg gag gtg							1536
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Met Leu Lys							
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<210> 66

<211> 515

<212> PRT

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 66

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Ser Ala Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
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Glu Trp Val Gly Glu Ile Leu Pro Gly Ser Asn Asn Ser Arg Tyr Asn
65 70 75 80

Glu Lys Phe Lys Gly Arg Val Thr Val Thr Arg Asp Thr Ser Thr Asn
85 90 95

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
100 105 110

Tyr Tyr Cys Ala Arg Ser Tyr Asp Phe Ala Trp Phe Ala Tyr Trp Gly
115 120 125

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
130 135 140

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145 150 155 160

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
165 170 175

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
180 185 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
195 200 205

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
210 215 220

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
225 230 235 240

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Gly Gly Leu
245 250 255

Lys Ile Ala Ala Phe Asn Ile Gln Thr Phe Gly Glu Thr Lys Met Ser
260 265 270

Asn Ala Thr Leu Val Ser Tyr Ile Val Gln Ile Leu Ser Arg Tyr Asp
275 280 285

Ile Ala Leu Val Gln Glu Val Arg Asp Ser His Leu Thr Ala Val Gly
290 295 300

Lys Leu Leu Asp Asn Leu Asn Gln Asp Ala Pro Asp Thr Tyr His Tyr
305 310 315 320

Val Val Ser Glu Pro Leu Gly Arg Asn Ser Tyr Lys Glu Arg Tyr Leu
325 330 335

Phe Val Tyr Arg Pro Asp Gln Val Ser Ala Val Asp Ser Tyr Tyr Tyr
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Asp Asp Gly Cys Glu Pro Cys Gly Asn Asp Thr Phe Asn Arg Glu Pro
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Ala Ile Val Arg Phe Phe Ser Arg Phe Thr Glu Val Arg Glu Phe Ala
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Ile Val Pro Leu His Ala Ala Pro Gly Asp Ala Val Ala Glu Ile Asp
 385 390 395 400

Ala Leu Tyr Asp Val Tyr Leu Asp Val Gln Glu Lys Trp Gly Leu Glu
 405 410 415

Asp Val Met Leu Met Gly Asp Phe Asn Ala Gly Cys Ser Tyr Val Arg
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Pro Ser Gln Trp Ser Ser Ile Arg Leu Trp Thr Ser Pro Thr Phe Gln
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Trp Leu Ile Pro Asp Ser Ala Asp Thr Thr Ala Thr Pro Thr His Cys
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Ala Tyr Asp Arg Ile Val Val Ala Gly Met Leu Leu Arg Gly Ala Val
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Val Pro Asp Ser Ala Leu Pro Phe Asn Phe Gln Ala Ala Tyr Gly Leu
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Met Leu Lys
 515

<210> 67

<211> 1566

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 67
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<210> 68

<211> 1566

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 68

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<210> 69

<211> 1575

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 69

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 gggagcggcg ggctgaagat cgcagccttc aacatccaga catthtgggga gaccaagatg 840
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<210> 70

<211> 1566

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<220>

<221> CDS

<222> (1)..(1566)

<223>

<400> 70

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1 5 10 15

gtc cac tcc cag gtg cag ctg gtg cag tct ggg gca gag gtg aaa aag 96
Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

cct ggg gcc tca gtg aag gtg tcc tgc aag gct tct ggc tac acc ttc 144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45

agt gcc tac tgg ata gag tgg gtg cgc cag gct cca gga aag ggc ctc 192
Ser Ala Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu

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gag aag ttc aag ggc cga gtg aca gtc act aga gac aca tcc aca aac Glu Lys Phe Lys Gly Arg Val Thr Val Thr Arg Asp Thr Ser Thr Asn 85 90 95			288
aca gcc tac atg gag ctc agc agc ctg agg tct gag gac aca gcc gtc Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val 100 105 110			336
tat tac tgt gca aga tcc tac gac ttt gcc tgg ttt gct tac tgg ggc Tyr Tyr Cys Ala Arg Ser Tyr Asp Phe Ala Trp Phe Ala Tyr Trp Gly 115 120 125			384
caa ggg act ctg gtc aca gtc tcc tca gcc tcc acc aag ggc cca tcg Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser 130 135 140			432
gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala 145 150 155 160			480
gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val 165 170 175			528
tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct Ser Trp Asn Ser Gly Ala Leu Thr Ser Ser Gly Val His Thr Phe Pro Ala 180 185 190			576
gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val 195 200 205			624
ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His 210 215 220			672
aag ccc agc aac acc aag gtg gac aag aaa gtt gag ccc aaa tct tgt Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys 225 230 235 240			720
gac aaa act cac aca tgc tgt gtg gag tgc cca ccg tgc cca gca cct Asp Lys Thr His Thr Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro 245 250 255			768
gaa ggg agc ggc ggg ctg aag atc gca gcc ttc aac atc cag aca ttt Glu Gly Ser Gly Gly Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr Phe 260 265 270			816
ggg gag acc aag atg tcc aat gcc acc ctc gtc agc tac att gtg cag Gly Glu Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val Gln 275 280 285			864
atc ctg agc cgc tac gac atc gcc ctg gtc cag gag gtc aga gac agc			912

Ile 290	Leu	Ser	Arg	Tyr	Asp	Ile 295	Ala	Leu	Val	Gln	Glu 300	Val	Arg	Asp	Ser	
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cca Pro	gac Asp	acc Thr	tat Tyr	cac His 325	tac Tyr	gtg Val	gtc Val	agt Ser	gag Glu 330	cca Pro	ctg Leu	gga Gly	cgg Arg	aac Asn 335	agc Ser	1008
tat Tyr	aag Lys	gag Glu	cgc Arg 340	tac Tyr	ctg Leu	ttc Phe	gtg Val	tac Tyr 345	agg Arg	cct Pro	gac Asp	cag Gln	gtg Val 350	tct Ser	gcg Ala	1056
gtg Val	gac Asp	agc Ser 355	tac Tyr	tac Tyr	tac Tyr	gat Asp	gat Asp 360	ggc Gly	tgc Cys	gag Glu	ccc Pro	tgc Cys 365	ggg Gly	aac Asn	gac Asp	1104
acc Thr	ttc Phe 370	aac Asn	cga Arg	gag Glu	cca Pro	gcc Ala 375	att Ile	gtc Val	agg Arg	ttc Phe	ttc Phe 380	tcc Ser	cgg Arg	ttc Phe	aca Thr	1152
gag Glu 385	gtc Val	agg Arg	gag Glu	ttt Phe	gcc Ala 390	att Ile	gtt Val	ccc Pro	ctg Leu	cat His 395	gcg Ala	gcc Ala	ccg Pro	ggg Gly	gac Asp 400	1200
gca Ala	gta Val	gcc Ala	gag Glu	atc Ile 405	gac Asp	gct Ala	ctc Leu	tat Tyr	gac Asp 410	gtc Val	tac Tyr	ctg Leu	gat Asp	gtc Val 415	caa Gln	1248
gag Glu	aaa Lys	tgg Trp	ggc Gly 420	ttg Leu	gag Glu	gac Asp	gtc Val	atg Met 425	ttg Leu	atg Met	ggc Gly	gac Asp	ttc Phe 430	aat Asn	gcg Ala	1296
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aca Thr	agc Ser 450	ccc Pro	acc Thr	ttc Phe	cag Gln	tgg Trp 455	ctg Leu	atc Ile	ccc Pro	gac Asp	agc Ser 460	gct Ala	gac Asp	acc Thr	aca Thr	1392
gct Ala 465	aca Thr	ccc Pro	acg Thr	cac His	tgt Cys 470	gcc Ala	tat Tyr	gac Asp	agg Arg	atc Ile 475	gtg Val	gtt Val	gca Ala	ggg Gly	atg Met 480	1440
ctg Leu	ctc Leu	cga Arg	ggg Gly	gcc Ala 485	gtt Val	gtt Val	ccc Pro	gac Asp	tcg Ser 490	gct Ala	ctt Leu	ccc Pro	ttt Phe	aac Asn 495	ttc Phe	1488
cag Gln	gct Ala	gcc Ala	tat Tyr 500	ggc Gly	ctg Leu	agt Ser	gac Asp	caa Gln 505	ctg Leu	gcc Ala	caa Gln	gcc Ala	atc Ile 510	agt Ser	gac Asp	1536
cac His	tat Tyr	cca Pro 515	gtg Val	gag Glu	gtg Val	atg Met	ctg Leu 520	aag Lys	tga							1566

<210> 71

<211> 521

<212> PRT

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 71

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Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
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Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45

Ser Ala Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
50 55 60

Glu Trp Val Gly Glu Ile Leu Pro Gly Ser Asn Asn Ser Arg Tyr Asn
65 70 75 80

Glu Lys Phe Lys Gly Arg Val Thr Val Thr Arg Asp Thr Ser Thr Asn
85 90 95

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
100 105 110

Tyr Tyr Cys Ala Arg Ser Tyr Asp Phe Ala Trp Phe Ala Tyr Trp Gly
115 120 125

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
130 135 140

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145 150 155 160

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
165 170 175

Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala
			180					185					190		
Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val
		195					200					205			
Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His
	210					215					220				
Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys
225					230					235					240
Asp	Lys	Thr	His	Thr	Cys	Cys	Val	Glu	Cys	Pro	Pro	Cys	Pro	Ala	Pro
				245					250					255	
Glu	Gly	Ser	Gly	Gly	Leu	Lys	Ile	Ala	Ala	Phe	Asn	Ile	Gln	Thr	Phe
			260					265					270		
Gly	Glu	Thr	Lys	Met	Ser	Asn	Ala	Thr	Leu	Val	Ser	Tyr	Ile	Val	Gln
		275					280					285			
Ile	Leu	Ser	Arg	Tyr	Asp	Ile	Ala	Leu	Val	Gln	Glu	Val	Arg	Asp	Ser
	290					295					300				
His	Leu	Thr	Ala	Val	Gly	Lys	Leu	Leu	Asp	Asn	Leu	Asn	Gln	Asp	Ala
305					310					315					320
Pro	Asp	Thr	Tyr	His	Tyr	Val	Val	Ser	Glu	Pro	Leu	Gly	Arg	Asn	Ser
				325					330					335	
Tyr	Lys	Glu	Arg	Tyr	Leu	Phe	Val	Tyr	Arg	Pro	Asp	Gln	Val	Ser	Ala
			340					345					350		
Val	Asp	Ser	Tyr	Tyr	Tyr	Asp	Asp	Gly	Cys	Glu	Pro	Cys	Gly	Asn	Asp
		355					360					365			
Thr	Phe	Asn	Arg	Glu	Pro	Ala	Ile	Val	Arg	Phe	Phe	Ser	Arg	Phe	Thr
	370					375					380				
Glu	Val	Arg	Glu	Phe	Ala	Ile	Val	Pro	Leu	His	Ala	Ala	Pro	Gly	Asp
385					390					395					400
Ala	Val	Ala	Glu	Ile	Asp	Ala	Leu	Tyr	Asp	Val	Tyr	Leu	Asp	Val	Gln

105

	405		410		415
Glu Lys Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn Ala					
	420		425		430
Gly Cys Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu Trp					
	435		440		445
Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr Thr					
	450		455		460
Ala Thr Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly Met					
	465		470		475
					480
Leu Leu Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn Phe					
	485		490		495
Gln Ala Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp					
	500		505		510
His Tyr Pro Val Glu Val Met Leu Lys					
	515		520		

<210> 72

<211> 1560

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 72

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tgcaaggctt ctggctacac cttcagtgcc tactggatag agtgggtgcg ccaggctcca	180
ggaaagggcc tcgagtgggt cggagagatt ttacctggaa gtaataattc tagatacaat	240
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gagctcagca gcctgaggtc tgaggacaca gccgtctatt actgtgcaag atcctacgac	360
tttgcttggt ttgcttactg gggccaaggg actctgggtca cagtctcctc agcctccacc	420

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ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac      600
tccttcagca gcgtgggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc      660
aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt      720
gacaaaactc acacatgctg tgtggagtgcc ccaccgtgcc cagcacctga aggcgggctg      780
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gccgagatcg acgtctctta tgacgtctac ctggatgtcc aagagaaatg gggcttggag     1260
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tcatccatcc gcctgtggac aagccccacc ttccagtggc tgatccccga cagcgctgac     1380
accacagcta caccacgca ctgtgcctat gacaggatcg tggttgcagg gatgctgctc     1440
cgagggggccg ttgttcccga ctcggtcttt ccctttaact tccaggctgc ctatggcctg     1500
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<210> 73

<211> 1560

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 73

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ggaaagggcc	tcgagtgggt	cggagagatt	ttacctggaa	gtaataattc	tagatacaat	240
gagaagttca	agggccgagt	gacagtcact	agagacacat	ccacaaacac	agcctacatg	300
gagctcagca	gcctgaggtc	tgaggacaca	gccgtctatt	actgtgcaag	atcctacgac	360
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cgagggggccg	ttgttcccga	ctcggtctct	ccctttaact	tccaggctgc	ctatggcctg	1500
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<210> 74

<211> 1569

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 74

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gacgcagtag ccgagatcga cgctctctat gacgtctacc tggatgtcca agagaaatgg     1260
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tcccagtggt catccatccg cctgtggaca agccccacct tccagtggtt gatccccgac     1380
agcgctgaca ccacagctac acccagcacac tgtgcctatg acaggatcgt ggttgcaggg     1440
atgctgctcc gaggggcccgt tgttcccagc tcggctcttc cttttaactt ccaggctgcc     1500
tatggcctga gtgaccaact ggcccaagcc atcagtgacc actatccagt ggaggtgatg     1560
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<210> 75

<211> 1560

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<220>

<221> CDS

<222> (1)..(1560)

<223>

<400> 75

atg gga tgg agc tgt atc atc ctc ttc ttg gta gca aca gct aca ggt	48
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly	
1 5 10 15	

gtc cac tcc cag gtg cag ctg gtg cag tct ggg gca gag gtg aaa aag	96
Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys	
20 25 30	

cct ggg gcc tca gtg aag gtg tcc tgc aag gct tct ggc tac acc ttc	144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe	
35 40 45	

agt gcc tac tgg ata gag tgg gtg cgc cag gct cca gga aag ggc ctc	192
Ser Ala Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu	
50 55 60	

gag tgg gtc gga gag att tta cct gga agt aat aat tct aga tac aat	240
Glu Trp Val Gly Glu Ile Leu Pro Gly Ser Asn Asn Ser Arg Tyr Asn	
65 70 75 80	

gag aag ttc aag ggc cga gtg aca gtc act aga gac aca tcc aca aac	288
Glu Lys Phe Lys Gly Arg Val Thr Val Thr Arg Asp Thr Ser Thr Asn	
85 90 95	

aca gcc tac atg gag ctc agc agc ctg agg tct gag gac aca gcc gtc	336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val	
100 105 110	

tat tac tgt gca aga tcc tac gac ttt gcc tgg ttt gct tac tgg ggc	384
Tyr Tyr Cys Ala Arg Ser Tyr Asp Phe Ala Trp Phe Ala Tyr Trp Gly	
115 120 125	

caa ggg act ctg gtc aca gtc tcc tca gcc tcc acc aag ggc cca tcg	432
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Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	
	130					135					140					
gtc	ttc	ccc	ctg	gca	ccc	tcc	tcc	aag	agc	acc	tct	ggg	ggc	aca	gcg	480
Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	
145					150					155					160	
gcc	ctg	ggc	tgc	ctg	gtc	aag	gac	tac	ttc	ccc	gaa	ccg	gtg	acg	gtg	528
Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	
				165					170					175		
tcg	tgg	aac	tca	ggc	gcc	ctg	acc	agc	ggc	gtg	cac	acc	ttc	ccg	gct	576
Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	
			180					185					190			
gtc	cta	cag	tcc	tca	gga	ctc	tac	tcc	ctc	agc	agc	gtg	gtg	acc	gtg	624
Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	
		195					200					205				
ccc	tcc	agc	agc	ttg	ggc	acc	cag	acc	tac	atc	tgc	aac	gtg	aat	cac	672
Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	
	210					215					220					
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Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	
225					230					235					240	
gac	aaa	act	cac	aca	tgc	tgt	gtg	gag	tgc	cca	ccg	tgc	cca	gca	cct	768
Asp	Lys	Thr	His	Thr	Cys	Cys	Val	Glu	Cys	Pro	Pro	Cys	Pro	Ala	Pro	
				245					250					255		
gaa	ggc	ggg	ctg	aag	atc	gca	gcc	ttc	aac	atc	cag	aca	ttt	ggg	gag	816
Glu	Gly	Gly	Leu	Lys	Ile	Ala	Ala	Phe	Asn	Ile	Gln	Thr	Phe	Gly	Glu	
			260					265					270			
acc	aag	atg	tcc	aat	gcc	acc	ctc	gtc	agc	tac	att	gtg	cag	atc	ctg	864
Thr	Lys	Met	Ser	Asn	Ala	Thr	Leu	Val	Ser	Tyr	Ile	Val	Gln	Ile	Leu	
		275					280					285				
agc	cgc	tac	gac	atc	gcc	ctg	gtc	cag	gag	gtc	aga	gac	agc	cac	ctg	912
Ser	Arg	Tyr	Asp	Ile	Ala	Leu	Val	Gln	Glu	Val	Arg	Asp	Ser	His	Leu	
	290					295					300					
act	gcc	gtg	ggg	aag	ctg	ctg	gac	aac	ctc	aat	cag	gac	gca	cca	gac	960
Thr	Ala	Val	Gly	Lys	Leu	Leu	Asp	Asn	Leu	Asn	Gln	Asp	Ala	Pro	Asp	
305					310					315					320	
acc	tat	cac	tac	gtg	gtc	agt	gag	cca	ctg	gga	cgg	aac	agc	tat	aag	1008
Thr	Tyr	His	Tyr	Val	Val	Ser	Glu	Pro	Leu	Gly	Arg	Asn	Ser	Tyr	Lys	
				325					330					335		
gag	cgc	tac	ctg	ttc	gtg	tac	agg	cct	gac	cag	gtg	tct	gcg	gtg	gac	1056
Glu	Arg	Tyr	Leu	Phe	Val	Tyr	Arg	Pro	Asp	Gln	Val	Ser	Ala	Val	Asp	
			340					345					350			
agc	tac	tac	tac	gat	gat	ggc	tgc	gag	ccc	tgc	ggg	aac	gac	acc	ttc	1104
Ser	Tyr	Tyr	Tyr	Asp	Asp	Gly	Cys	Glu	Pro	Cys	Gly	Asn	Asp	Thr	Phe	
		355					360					365				

aac cga gag cca gcc att gtc agg ttc ttc tcc cgg ttc aca gag gtc	1152
Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe Thr Glu Val	
370 375 380	
agg gag ttt gcc att gtt ccc ctg cat gcg gcc ccg ggg gac gca gta	1200
Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly Asp Ala Val	
385 390 395 400	
gcc gag atc gac gct ctc tat gac gtc tac ctg gat gtc caa gag aaa	1248
Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val Gln Glu Lys	
405 410 415	
tgg ggc ttg gag gac gtc atg ttg atg ggc gac ttc aat gcg ggc tgc	1296
Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn Ala Gly Cys	
420 425 430	
agc tat gtg aga ccc tcc cag tgg tca tcc atc cgc ctg tgg aca agc	1344
Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu Trp Thr Ser	
435 440 445	
ccc acc ttc cag tgg ctg atc ccc gac agc gct gac acc aca gct aca	1392
Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr Thr Ala Thr	
450 455 460	
ccc acg cac tgt gcc tat gac agg atc gtg gtt gca ggg atg ctg ctc	1440
Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly Met Leu Leu	
465 470 475 480	
cga ggg gcc gtt gtt ccc gac tcg gct ctt ccc ttt aac ttc cag gct	1488
Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn Phe Gln Ala	
485 490 495	
gcc tat ggc ctg agt gac caa ctg gcc caa gcc atc agt gac cac tat	1536
Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp His Tyr	
500 505 510	
cca gtg gag gtg atg ctg aag tga	1560
Pro Val Glu Val Met Leu Lys	
515	

<210> 76

<211> 519

<212> PRT

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 76

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			20					25					30					
Pro	Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe			
		35					40					45						
Ser	Ala	Tyr	Trp	Ile	Glu	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu			
	50					55					60							
Glu	Trp	Val	Gly	Glu	Ile	Leu	Pro	Gly	Ser	Asn	Asn	Ser	Arg	Tyr	Asn			
65					70					75					80			
Glu	Lys	Phe	Lys	Gly	Arg	Val	Thr	Val	Thr	Arg	Asp	Thr	Ser	Thr	Asn			
				85					90					95				
Thr	Ala	Tyr	Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val			
			100					105					110					
Tyr	Tyr	Cys	Ala	Arg	Ser	Tyr	Asp	Phe	Ala	Trp	Phe	Ala	Tyr	Trp	Gly			
		115					120					125						
Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser			
	130					135					140							
Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala			
145					150					155					160			
Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val			
				165					170					175				
Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala			
			180					185					190					
Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val			
		195					200					205						
Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His			
	210					215					220							
Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys			
225					230					235					240			
Asp	Lys	Thr	His	Thr	Cys	Cys	Val	Glu	Cys	Pro	Pro	Cys	Pro	Ala	Pro			

245										250					255				
Glu	Gly	Gly	Leu	Lys	Ile	Ala	Ala	Phe	Asn	Ile	Gln	Thr	Phe	Gly	Glu				
			260					265					270						
Thr	Lys	Met	Ser	Asn	Ala	Thr	Leu	Val	Ser	Tyr	Ile	Val	Gln	Ile	Leu				
		275					280					285							
Ser	Arg	Tyr	Asp	Ile	Ala	Leu	Val	Gln	Glu	Val	Arg	Asp	Ser	His	Leu				
	290					295					300								
Thr	Ala	Val	Gly	Lys	Leu	Leu	Asp	Asn	Leu	Asn	Gln	Asp	Ala	Pro	Asp				
305					310					315					320				
Thr	Tyr	His	Tyr	Val	Val	Ser	Glu	Pro	Leu	Gly	Arg	Asn	Ser	Tyr	Lys				
				325					330					335					
Glu	Arg	Tyr	Leu	Phe	Val	Tyr	Arg	Pro	Asp	Gln	Val	Ser	Ala	Val	Asp				
			340					345					350						
Ser	Tyr	Tyr	Tyr	Asp	Asp	Gly	Cys	Glu	Pro	Cys	Gly	Asn	Asp	Thr	Phe				
		355					360					365							
Asn	Arg	Glu	Pro	Ala	Ile	Val	Arg	Phe	Phe	Ser	Arg	Phe	Thr	Glu	Val				
	370					375					380								
Arg	Glu	Phe	Ala	Ile	Val	Pro	Leu	His	Ala	Ala	Pro	Gly	Asp	Ala	Val				
385					390					395					400				
Ala	Glu	Ile	Asp	Ala	Leu	Tyr	Asp	Val	Tyr	Leu	Asp	Val	Gln	Glu	Lys				
				405					410					415					
Trp	Gly	Leu	Glu	Asp	Val	Met	Leu	Met	Gly	Asp	Phe	Asn	Ala	Gly	Cys				
			420					425					430						
Ser	Tyr	Val	Arg	Pro	Ser	Gln	Trp	Ser	Ser	Ile	Arg	Leu	Trp	Thr	Ser				
		435					440					445							
Pro	Thr	Phe	Gln	Trp	Leu	Ile	Pro	Asp	Ser	Ala	Asp	Thr	Thr	Ala	Thr				
	450					455					460								
Pro	Thr	His	Cys	Ala	Tyr	Asp	Arg	Ile	Val	Val	Ala	Gly	Met	Leu	Leu				
465					470					475					480				

Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn Phe Gln Ala
485 490 495

Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp His Tyr
500 505 510

Pro Val Glu Val Met Leu Lys
515

<210> 77

<211> 1560

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 77

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gtgcagctgg	tgcagtctgg	ggcagaggtg	aaaaagcctg	gggcctcagt	gaaggtgtcc	120
tgcaaggctt	ctggctacac	cttcagtgcc	tactggatag	agtgggtgcg	ccagggtcca	180
ggaaagggcc	tcgagtgggt	cggagagatt	ttacctggaa	gtaataattc	tagatacaat	240
gagaagttca	agggccgagt	gacagtcact	agagacacat	ccacaaacac	agcctacatg	300
gagctcagca	gcctgaggtc	tgaggacaca	gccgtctatt	actgtgcaag	atcctacgac	360
tttgcttgg	ttgcttactg	gggccaaggg	actctgggtca	cagtctcctc	agcctccacc	420
aagggcccat	cggctcttccc	cctggcacccc	tcctccaaga	gcacctctgg	gggcacagcg	480
gccctgggct	gcctgggtcaa	ggactacttc	cccgaaccgg	tgacgggtgtc	gtggaactca	540
ggcgccctga	ccagcggcgt	gcacaccttc	ccggctgtcc	tacagtcctc	aggactctac	600
tcctcagca	gcgtgggtgac	cgtgccctcc	agcagcttgg	gcaccagac	ctacatctgc	660
aacgtgaatc	acaagcccag	caacaccaag	gtggacaaga	aagttgagcc	caaatcttgt	720
gacaaaactc	acacatgctg	tgtggagtg	ccaccgtgcc	cagcacctga	aggcaggctg	780
aagatcgag	ccttcaacat	ccagacattt	ggggagacca	agatgtccaa	tgccaccctc	840
gtcagctaca	ttgtgcagat	cctgagccgc	tacgacatcg	ccctgggtcca	ggaggtcaga	900
gacagccacc	tgactgccgt	ggagaagctg	ctggacaacc	tcaatcagga	cgcaccagac	960

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acctatcact acgtggtcag tgagccactg ggacggaaca gctataagga gcgctacctg 1020
ttcgtgtaca ggccctgacca ggtgtctgcg gtggacagct actactacga tgatggctgc 1080
gagccctgcg ggaacgacac cttcaaccga gagccagcca ttgtcagggtt cttctcccgg 1140
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gccgagatcg acgtctctta tgacgtctac ctggatgtcc aagagaaatg gggcttggag 1260
gacgtcatgt tgatgggcga cttcaatgcg ggctgcagct atgtgagacc ctcccagtgg 1320
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accacagcta caccacgca ctgtgcctat gacaggatcg tggttgcagg gatgctgctc 1440
cgagggggccg ttgttcccga ctcggtcttt ccttttaact tccaggctgc ctatggcctg 1500
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<210> 78

<211> 1560

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 78

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tgcaaggctt ctggctacac cttcagtgcc tactggatag agtgggtgcg ccagggtcca 180
ggaaagggcc tcgagtgggt cggagagatt ttacctggaa gtaataattc tagatacaat 240
gagaagttca agggccgagt gacagtcact agagacacat ccacaaacac agcctacatg 300
gagctcagca gcctgaggtc tgaggacaca gccgtctatt actgtgcaag atcctacgac 360
tttgccctgg ttgcttactg gggccaaggg actctgggtca cagtctcctc agcctccacc 420
aaggggcccat cggctcttccc cctggcacc cctccaaga gcacctctgg gggcacagcg 480
gcctggggt gcctgggtcaa ggactacttc cccgaaccgg tgacgggtgtc gtggaactca 540
ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac 600
tcctcagca gcgtgggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc 660
aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt 720

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gacaaaactc acacatgctg tgtcgagtgt ccaccgtgtc cagcaccaga gggcaggctg      780
aagatcgcag ccttcaacat ccagacattt ggggagacca agatgtccaa tgccaccctc      840
gtcagctaca ttgtgcagat cctgagccgc tacgacatcg ccctgggtcca ggaggtcaga      900
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acctatcact acgtgggtcag tgagccactg ggacggaaca gctataagga gcgctacctg     1020
ttcgtgtaca ggcctgacca ggtgtctgcg gtggacagct actactacga tgatggctgc     1080
gagccctgcg ggaacgacac cttcaaccga gagccagcca ttgtcagggtt cttctcccgg     1140
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tcatecatcc gcctgtggac aagccccacc ttccagtggc tgatccccga cagcgctgac     1380
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cgagggggccg ttgttcccga ctcggtctct cccctttaact tccaggctgc ctatggcctg     1500
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<210> 79

<211> 1560

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<220>

<221> CDS

<222> (1)..(1560)

<223>

<400> 79

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1           5           10           15

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gtc	cac	tcc	cag	gtg	cag	ctg	gtg	cag	tct	ggg	gca	gag	gtg	aaa	aag	96
Val	His	Ser	Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	
			20					25					30			
cct	ggg	gcc	tca	gtg	aag	gtg	tcc	tgc	aag	gct	tct	ggc	tac	acc	ttc	144
Pro	Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	
		35					40					45				
agt	gcc	tac	tgg	ata	gag	tgg	gtg	cgc	cag	gct	cca	gga	aag	ggc	ctc	192
Ser	Ala	Tyr	Trp	Ile	Glu	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	
	50					55					60					
gag	tgg	gtc	gga	gag	att	tta	cct	gga	agt	aat	aat	tct	aga	tac	aat	240
Glu	Trp	Val	Gly	Glu	Ile	Leu	Pro	Gly	Ser	Asn	Asn	Ser	Arg	Tyr	Asn	
65					70					75					80	
gag	aag	ttc	aag	ggc	cga	gtg	aca	gtc	act	aga	gac	aca	tcc	aca	aac	288
Glu	Lys	Phe	Lys	Gly	Arg	Val	Thr	Val	Thr	Arg	Asp	Thr	Ser	Thr	Asn	
				85					90					95		
aca	gcc	tac	atg	gag	ctc	agc	agc	ctg	agg	tct	gag	gac	aca	gcc	gtc	336
Thr	Ala	Tyr	Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	
			100					105						110		
tat	tac	tgt	gca	aga	tcc	tac	gac	ttt	gcc	tgg	ttt	gct	tac	tgg	ggc	384
Tyr	Tyr	Cys	Ala	Arg	Ser	Tyr	Asp	Phe	Ala	Trp	Phe	Ala	Tyr	Trp	Gly	
		115					120					125				
caa	ggg	act	ctg	gtc	aca	gtc	tcc	tca	gcc	tcc	acc	aag	ggc	cca	tcg	432
Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	
	130					135					140					
gtc	ttc	ccc	ctg	gca	ccc	tcc	tcc	aag	agc	acc	tct	ggg	ggc	aca	gcg	480
Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	
145					150					155					160	
gcc	ctg	ggc	tgc	ctg	gtc	aag	gac	tac	ttc	ccc	gaa	ccg	gtg	acg	gtg	528
Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	
				165					170					175		
tcg	tgg	aac	tca	ggc	gcc	ctg	acc	agc	ggc	gtg	cac	acc	ttc	ccg	gct	576
Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	
			180					185					190			
gtc	cta	cag	tcc	tca	gga	ctc	tac	tcc	ctc	agc	agc	gtg	gtg	acc	gtg	624
Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	
		195					200					205				
ccc	tcc	agc	agc	ttg	ggc	acc	cag	acc	tac	atc	tgc	aac	gtg	aat	cac	672
Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	
	210					215					220					
aag	ccc	agc	aac	acc	aag	gtg	gac	aag	aaa	gtt	gag	ccc	aaa	tct	tgt	720
Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	
225					230					235					240	
gac	aaa	act	cac	aca	tgc	tgt	gtg	gag	tgc	cca	ccg	tgc	cca	gca	cct	768
Asp	Lys	Thr	His	Thr	Cys	Cys	Val	Glu	Cys	Pro	Pro	Cys	Pro	Ala	Pro	
				245					250					255		

gaa ggc agg ctg aag atc gca gcc ttc aac atc cag aca ttt ggg gag	816
Glu Gly Arg Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr Phe Gly Glu	
260 265 270	
acc aag atg tcc aat gcc acc ctc gtc agc tac att gtg cag atc ctg	864
Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val Gln Ile Leu	
275 280 285	
agc cgc tac gac atc gcc ctg gtc cag gag gtc aga gac agc cac ctg	912
Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp Ser His Leu	
290 295 300	
act gcc gtg gag aag ctg ctg gac aac ctc aat cag gac gca cca gac	960
Thr Ala Val Glu Lys Leu Leu Asp Asn Leu Asn Gln Asp Ala Pro Asp	
305 310 315 320	
acc tat cac tac gtg gtc agt gag cca ctg gga cgg aac agc tat aag	1008
Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn Ser Tyr Lys	
325 330 335	
gag cgc tac ctg ttc gtg tac agg cct gac cag gtg tct gcg gtg gac	1056
Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser Ala Val Asp	
340 345 350	
agc tac tac tac gat gat ggc tgc gag ccc tgc ggg aac gac acc ttc	1104
Ser Tyr Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn Asp Thr Phe	
355 360 365	
aac cga gag cca gcc att gtc agg ttc ttc tcc cgg ttc aca gag gtc	1152
Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe Thr Glu Val	
370 375 380	
agg gag ttt gcc att gtt ccc ctg cat gcg gcc ccg ggg gac gca gta	1200
Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly Asp Ala Val	
385 390 395 400	
gcc gag atc gac gct ctc tat gac gtc tac ctg gat gtc caa gag aaa	1248
Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val Gln Glu Lys	
405 410 415	
tgg ggc ttg gag gac gtc atg ttg atg ggc gac ttc aat gcg ggc tgc	1296
Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn Ala Gly Cys	
420 425 430	
agc tat gtg aga ccc tcc cag tgg tca tcc atc cgc ctg tgg aca agc	1344
Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu Trp Thr Ser	
435 440 445	
ccc acc ttc cag tgg ctg atc ccc gac agc gct gac acc aca gct aca	1392
Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr Thr Ala Thr	
450 455 460	
ccc acg cac tgt gcc tat gac agg atc gtg gtt gca ggg atg ctg ctc	1440
Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly Met Leu Leu	
465 470 475 480	
cga ggg gcc gtt gtt ccc gac tcg gct ctt ccc ttt aac ttc cag gct	1488
Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn Phe Gln Ala	

	485	490	495	
gcc tat ggc ctg agt gac caa ctg gcc caa gcc atc agt gac cac tat				1536
Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp His Tyr				
	500	505	510	
cca gtg gag gtg atg ctg aag tga				1560
Pro Val Glu Val Met Leu Lys				
	515			

<210> 80

<211> 519

<212> PRT

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 80

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1 5 10 15

Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45

Ser Ala Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
50 55 60

Glu Trp Val Gly Glu Ile Leu Pro Gly Ser Asn Asn Ser Arg Tyr Asn
65 70 75 80

Glu Lys Phe Lys Gly Arg Val Thr Val Thr Arg Asp Thr Ser Thr Asn
85 90 95

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
100 105 110

Tyr Tyr Cys Ala Arg Ser Tyr Asp Phe Ala Trp Phe Ala Tyr Trp Gly
115 120 125

Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	130	135	140	
Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	145	150	155	160
Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	165	170	175	
Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	180	185	190	
Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	195	200	205	
Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	210	215	220	
Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	225	230	235	240
Asp	Lys	Thr	His	Thr	Cys	Cys	Val	Glu	Cys	Pro	Pro	Cys	Pro	Ala	Pro	245	250	255	
Glu	Gly	Arg	Leu	Lys	Ile	Ala	Ala	Phe	Asn	Ile	Gln	Thr	Phe	Gly	Glu	260	265	270	
Thr	Lys	Met	Ser	Asn	Ala	Thr	Leu	Val	Ser	Tyr	Ile	Val	Gln	Ile	Leu	275	280	285	
Ser	Arg	Tyr	Asp	Ile	Ala	Leu	Val	Gln	Glu	Val	Arg	Asp	Ser	His	Leu	290	295	300	
Thr	Ala	Val	Glu	Lys	Leu	Leu	Asp	Asn	Leu	Asn	Gln	Asp	Ala	Pro	Asp	305	310	315	320
Thr	Tyr	His	Tyr	Val	Val	Ser	Glu	Pro	Leu	Gly	Arg	Asn	Ser	Tyr	Lys	325	330	335	
Glu	Arg	Tyr	Leu	Phe	Val	Tyr	Arg	Pro	Asp	Gln	Val	Ser	Ala	Val	Asp	340	345	350	
Ser	Tyr	Tyr	Tyr	Asp	Asp	Gly	Cys	Glu	Pro	Cys	Gly	Asn	Asp	Thr	Phe	355	360	365	

Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe Thr Glu Val
 370 375 380

Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly Asp Ala Val
 385 390 395 400

Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val Gln Glu Lys
 405 410 415

Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn Ala Gly Cys
 420 425 430

Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu Trp Thr Ser
 435 440 445

Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr Thr Ala Thr
 450 455 460

Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly Met Leu Leu
 465 470 475 480

Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn Phe Gln Ala
 485 490 495

Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp His Tyr
 500 505 510

Pro Val Glu Val Met Leu Lys
 515

<210> 81

<211> 1578

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 81

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gtgcagctgg tgcagtctgg ggcagagggtg aaaaagcctg gggcctcagt gaaggtgtcc 120

tgcaaggctt ctggctacac cttcagtgcc tactggatag agtgggtgcg ccaggctcca	180
ggaaagggcc tcgagtgggt cggagagatt ttacctggaa gtaataattc tagatacaat	240
gagaagttca agggccgagt gacagtcact agagacacat ccacaaacac agcctacatg	300
gagctcagca gcctgaggtc tgaggacaca gccgtctatt actgtgcaag atcctacgac	360
tttgccctgggt ttgcttactg gggccaaggg actctgggtca cagtctcctc agcctccacc	420
aagggcccat cggctcttccc cctggcaccc tccccaaga gcacctctgg gggcacagcg	480
gccctgggct gcctgggtcaa ggactacttc cccgaaccgg tgacgggtgtc gtggaactca	540
ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac	600
tccctcagca gcgtgggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc	660
aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt	720
gacaaaactc acacatgccc accgtgccc gcacctgaag gcgggctgaa gatcgcagcc	780
ttcaacatcc agacatttgg ggagaccaag atgtccaatg ccaccctcgt cagctacatt	840
gtgcagatcc tgagccgcta cgacatcgcc ctgggtccagg aggtcagaga cagccacctg	900
actgccgtgg ggaagctgct ggacaacctc aatcaggacg caccagacac ctatcactac	960
gtggtcagtg agccactggg acggaacagc tataaggagc gctacctgtt cgtgtacagg	1020
cctgaccagg tgtctgcggt ggacagctac tactacgatg atggctgcga gccctgcggg	1080
aacgacacct tcaaccgaga gccagccatt gtcaggttct tctcccgggt cacagaggtc	1140
agggagtttg ccattgttcc cctgcatgcg gccccggggg acgcagtagc cgagatcgac	1200
gctctctatg acgtctacct ggatgtccaa gagaaatggg gcttggagga cgtcatgttg	1260
atgggcgact tcaatgcggg ctgcagctat gtgagaccct ccagtggtc atccatccgc	1320
ctgtggacaa gcccacctt ccagtggctg atccccgaca gcgctgacac cacagctaca	1380
cccacgcact gtgcctatga caggatcgtg gttgcaggga tgctgctccg aggggcccgtt	1440
gttcccgaact cggtctctcc ctttaacttc caggctgcct atggcctgag tgaccaactg	1500
gccaagcca tcagtacca ctatccagtg gaggtgatgc tgaagggggg cggacccaaa	1560
aagaagcgca aggtttga	1578

<210> 82

<211> 1578

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 82

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gtgcagctgg tgcagtctgg ggcagaggtg aaaaagcctg gggcctcagt gaaggtgtcc	120
tgcaaggctt ctggctacac cttcagtgcc tactggatag agtgggtgcg ccaggctcca	180
ggaaagggcc tcgagtgggt cggagagatt ttacctggaa gtaataattc tagatacaat	240
gagaagttca agggccgagt gacagtcact agagacacat ccacaaacac agcctacatg	300
gagctcagca gcctgaggtc tgaggacaca gccgtctatt actgtgcaag atcctacgac	360
tttgccctggg ttgcttactg gggccaaggg actctgggtca cagtctcctc agcctccacc	420
aaggggcccat cggtcttccc cctggcaccc tcttccaaga gcacctctgg gggcacagcg	480
gccctggggt gcctgggtcaa ggactacttc cccgaaccgg tgacgggtgtc gtggaactca	540
ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac	600
tcctcagca gcgtgggtgac cgtgccctcc agcagcttgg gcaccagac ctacatctgc	660
aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt	720
gacaaaactc acacatgtcc accgtgtcca gcaccagagg gcgggctgaa gatcgcagcc	780
ttcaacatcc agacatttgg ggagaccaag atgtccaatg ccaccctcgt cagctacatt	840
gtgcagatcc tgagccgcta cgacatcgcc ctggtccagg aggtcagaga cagccacctg	900
actgccgtgg ggaagctgct ggacaacctc aatcaggacg caccagacac ctatcactac	960
gtggtcagtg agccactggg acggaacagc tataaggagc gctacctgtt cgtgtacagg	1020
cctgaccagg tgtctgcggt ggacagctac tactacgatg atggctgcga gccctgcggg	1080
aacgacacct tcaaccgaga gccagccatt gtcaggttct tctcccgggt cacagaggtc	1140
agggagtttg ccattgttcc cctgcatgcg gccccggggg acgcagtagc cgagatcgac	1200
gctctctatg acgtctacct ggatgtccaa gagaaatggg gcttggagga cgtcatgttg	1260
atgggcgact tcaatgcggg ctgcagctat gtgagaccct ccagtggtc atccatccgc	1320
ctgtggacaa gcccacctt ccagtggctg atccccgaca gcgctgacac cacagctaca	1380
cccacgcact gtgcctatga caggatcgtg gttgcaggga tgctgctccg aggggcccgtt	1440
gttcccagact cggctcttcc ctttaacttc caggctgcct atggcctgag tgaccaactg	1500

gccaagcca tcagtgacca ctatccagtg gaggtgatgc tgaagggggg cggacccaaa 1560
aagaagcgca aggtttga 1578

<210> 83

<211> 1587

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 83

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cactcccagg tgcagctggg gcagctctgg gcagaggtga aaaagcctgg ggcctcagtg 120
aaggtgtcct gcaaggcttc tggctacacc ttcagtgccct actggataga gtgggtgcgc 180
caggctccag gaaagggcct cgagtgggtc ggagagattt tacctggaag taataattct 240
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gcctccacca agggcccatc ggtcttcccc ctggcacccct cctccaagag cacctctggg 480
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tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 600
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tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 720
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atcgcagcct tcaacatcca gacatttggg gagaccaaga tgtccaatgc caccctcgtc 840
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agccacctga ctgccgtggg gaagctgctg gacaacctca atcaggacgc accagacacc 960
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ccctgcggga acgacacctt caaccgagag ccagccattg tcaggttctt ctcccgggtc 1140
acagaggtca gggagtthgc cattgttccc ctgcatgcgg ccccggggga cgcagtagcc 1200


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gagatcgacg ctctctatga cgtctacctg gatgtccaag agaaatgggg cttggaggac 1260
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ggggccgttg ttcccgactc ggctcttccc tttaacttcc aggctgccta tggcctgagt 1500
gaccaactgg cccaagccat cagtgaccac tatccagtgg aggtgatgct gaaggggggc 1560
ggacccaaaa agaagcgcaa ggtttga 1587

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<210> 84

<211> 1578

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<220>

<221> CDS

<222> (1)..(1578)

<223>

<400> 84

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atg gga tgg agc tgt atc atc ctc ttc ttg gta gca aca gct aca ggt 48
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1 5 10 15

gtc cac tcc cag gtg cag ctg gtg cag tct ggg gca gag gtg aaa aag 96
Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

cct ggg gcc tca gtg aag gtg tcc tgc aag gct tct ggc tac acc ttc 144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45

agt gcc tac tgg ata gag tgg gtg cgc cag gct cca gga aag ggc ctc 192
Ser Ala Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
50 55 60

gag tgg gtc gga gag att tta cct gga agt aat aat tct aga tac aat 240
Glu Trp Val Gly Glu Ile Leu Pro Gly Ser Asn Asn Ser Arg Tyr Asn

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65				70				75				80				
gag Glu	aag Lys	ttc Phe	aag Lys	ggc Gly 85	cga Arg	gtg Val	aca Thr	gtc Val	act Thr 90	aga Arg	gac Asp	aca Thr	tcc Ser	aca Thr 95	aac Asn	288
aca Thr	gcc Ala	tac Tyr	atg Met 100	gag Glu	ctc Leu	agc Ser	agc Ser	ctg Leu 105	agg Arg	tct Ser	gag Glu	gac Asp	aca Thr 110	gcc Ala	gtc Val	336
tat Tyr	tac Tyr	tgt Cys 115	gca Ala	aga Arg	tcc Ser	tac Tyr	gac Asp 120	ttt Phe	gcc Ala	tgg Trp	ttt Phe	gct Ala 125	tac Tyr	tgg Trp	ggc Gly	384
caa Gln	ggg Gly 130	act Thr	ctg Leu	gtc Val	aca Thr	gtc Val 135	tcc Ser	tca Ser	gcc Ala	tcc Ser	acc Thr 140	aag Lys	ggc Gly	cca Pro	tcg Ser	432
gtc Val 145	ttc Phe	ccc Pro	ctg Leu	gca Ala	ccc Pro 150	tcc Ser	tcc Ser	aag Lys	agc Ser	acc Thr 155	tct Ser	ggg Gly	ggc Gly	aca Thr	gcg Ala 160	480
gcc Ala	ctg Leu	ggc Gly	tgc Cys 165	ctg Leu	gtc Val	aag Lys	gac Asp	tac Tyr 170	ttc Phe	ccc Pro	gaa Glu	ccg Pro	gtg Val 175	acg Thr	gtg Val	528
tcg Ser	tgg Trp	aac Asn 180	tca Ser	ggc Gly	gcc Ala	ctg Leu	acc Thr 185	agc Ser	ggc Gly	gtg Val	cac His	acc Thr	ttc Phe 190	ccg Pro	gct Ala	576
gtc Val	cta Leu 195	cag Gln	tcc Ser	tca Ser	gga Gly	ctc Leu	tac Tyr 200	tcc Ser	ctc Leu	agc Ser	agc Ser	gtg Val 205	gtg Val	acc Thr	gtg Val	624
ccc Pro 210	tcc Ser	agc Ser	agc Ser	ttg Leu	ggc Gly	acc Thr 215	cag Gln	acc Thr	tac Tyr	atc Ile	tgc Cys 220	aac Asn	gtg Val	aat Asn	cac His	672
aag Lys 225	ccc Pro	agc Ser	aac Asn	acc Thr	aag Lys 230	gtg Val	gac Asp	aag Lys	aaa Lys	gtt Val 235	gag Glu	ccc Pro	aaa Lys	tct Ser	tgt Cys 240	720
gac Asp	aaa Lys	act Thr	cac His 245	aca Thr	tgc Cys	cca Pro	ccg Pro	tgc Cys	cca Pro 250	gca Ala	cct Pro	gaa Glu	ggc Gly	ggg Gly 255	ctg Leu	768
aag Lys	atc Ile	gca Ala 260	gcc Ala	ttc Phe	aac Asn	atc Ile	cag Gln	aca Thr 265	ttt Phe	ggg Gly	gag Glu	acc Thr 270	aag Lys	atg Met	tcc Ser	816
aat Asn	gcc Ala 275	acc Thr	ctc Leu	gtc Val	agc Ser	tac Tyr	att Ile 280	gtg Val	cag Gln	atc Ile	ctg Leu 285	agc Ser	cgc Arg	tac Tyr	gac Asp	864
atc Ile 290	gcc Ala	ctg Leu	gtc Val	cag Gln	gag Glu	gtc Val 295	aga Arg	gac Asp	agc Ser	cac His	ctg Leu 300	act Thr	gcc Ala	gtg Val	ggg Gly	912
aaq	ctg	ctg	gac	aac	ctc	aat	caq	gac	gca	cca	gac	acc	tat	cac	tac	960

Lys 305	Leu	Leu	Asp	Asn	Leu 310	Asn	Gln	Asp	Ala	Pro 315	Asp	Thr	Tyr	His	Tyr 320	
gtg	gtc	agt	gag	cca	ctg	gga	cgg	aac	agc	tat	aag	gag	cgc	tac	ctg	1008
Val	Val	Ser	Glu	Pro 325	Leu	Gly	Arg	Asn	Ser 330	Tyr	Lys	Glu	Arg	Tyr 335	Leu	
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Phe	Val	Tyr	Arg 340	Pro	Asp	Gln	Val	Ser 345	Ala	Val	Asp	Ser	Tyr 350	Tyr	Tyr	
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Asp	Asp	Gly 355	Cys	Glu	Pro	Cys	Gly 360	Asn	Asp	Thr	Phe	Asn 365	Arg	Glu	Pro	
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Ala	Ile 370	Val	Arg	Phe	Phe	Ser 375	Arg	Phe	Thr	Glu	Val 380	Arg	Glu	Phe	Ala	
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Ile	Val	Pro	Leu	His 390	Ala	Ala	Pro	Gly	Asp 395	Ala	Val	Ala	Glu	Ile	Asp 400	
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Ala	Leu	Tyr	Asp 405	Val	Tyr	Leu	Asp	Val	Gln 410	Glu	Lys	Trp	Gly 415	Leu	Glu	
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Asp	Val	Met	Leu 420	Met	Gly	Asp	Phe 425	Asn	Ala	Gly	Cys	Ser	Tyr 430	Val	Arg	
ccc	tcc	cag	tgg	tca	tcc	atc	cgc	ctg	tgg	aca	agc	ccc	acc	ttc	cag	1344
Pro	Ser	Gln 435	Trp	Ser	Ser	Ile	Arg 440	Leu	Trp	Thr	Ser	Pro 445	Thr	Phe	Gln	
tgg	ctg	atc	ccc	gac	agc	gct	gac	acc	aca	gct	aca	ccc	acg	cac	tgt	1392
Trp	Leu 450	Ile	Pro	Asp	Ser	Ala 455	Asp	Thr	Thr	Ala	Thr 460	Pro	Thr	His	Cys	
gcc	tat	gac	agg	atc	gtg	gtt	gca	ggg	atg	ctg	ctc	cga	ggg	gcc	gtt	1440
Ala	Tyr	Asp	Arg	Ile 470	Val	Val	Ala	Gly	Met 475	Leu	Leu	Arg	Gly	Ala	Val 480	
gtt	ccc	gac	tgc	gct	ctt	ccc	ttt	aac	ttc	cag	gct	gcc	tat	ggc	ctg	1488
Val	Pro	Asp	Ser 485	Ala	Leu	Pro	Phe	Asn 490	Phe	Gln	Ala	Ala	Tyr	Gly 495	Leu	
agt	gac	caa	ctg	gcc	caa	gcc	atc	agt	gac	cac	tat	cca	gtg	gag	gtg	1536
Ser	Asp	Gln 500	Leu	Ala	Gln	Ala	Ile	Ser 505	Asp	His	Tyr	Pro 510	Val	Glu	Val	
atg	ctg	aag	ggg	ggc	gga	ccc	aaa	aag	aag	cgc	aag	gtt	tga			1578
Met	Leu	Lys 515	Gly	Gly	Gly	Pro	Lys 520	Lys	Lys	Arg	Lys	Val 525				

<211> 525

<212> PRT

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 85

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1 5 10 15

Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45

Ser Ala Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
50 55 60

Glu Trp Val Gly Glu Ile Leu Pro Gly Ser Asn Asn Ser Arg Tyr Asn
65 70 75 80

Glu Lys Phe Lys Gly Arg Val Thr Val Thr Arg Asp Thr Ser Thr Asn
85 90 95

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
100 105 110

Tyr Tyr Cys Ala Arg Ser Tyr Asp Phe Ala Trp Phe Ala Tyr Trp Gly
115 120 125

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
130 135 140

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145 150 155 160

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
165 170 175

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala

180					185					190					
Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val
		195					200					205			
Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His
	210					215					220				
Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys
225					230					235					240
Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Gly	Gly	Leu
				245					250					255	
Lys	Ile	Ala	Ala	Phe	Asn	Ile	Gln	Thr	Phe	Gly	Glu	Thr	Lys	Met	Ser
			260					265					270		
Asn	Ala	Thr	Leu	Val	Ser	Tyr	Ile	Val	Gln	Ile	Leu	Ser	Arg	Tyr	Asp
		275					280					285			
Ile	Ala	Leu	Val	Gln	Glu	Val	Arg	Asp	Ser	His	Leu	Thr	Ala	Val	Gly
	290					295					300				
Lys	Leu	Leu	Asp	Asn	Leu	Asn	Gln	Asp	Ala	Pro	Asp	Thr	Tyr	His	Tyr
305					310				315						320
Val	Val	Ser	Glu	Pro	Leu	Gly	Arg	Asn	Ser	Tyr	Lys	Glu	Arg	Tyr	Leu
				325					330					335	
Phe	Val	Tyr	Arg	Pro	Asp	Gln	Val	Ser	Ala	Val	Asp	Ser	Tyr	Tyr	Tyr
			340					345					350		
Asp	Asp	Gly	Cys	Glu	Pro	Cys	Gly	Asn	Asp	Thr	Phe	Asn	Arg	Glu	Pro
		355					360					365			
Ala	Ile	Val	Arg	Phe	Phe	Ser	Arg	Phe	Thr	Glu	Val	Arg	Glu	Phe	Ala
	370					375					380				
Ile	Val	Pro	Leu	His	Ala	Ala	Pro	Gly	Asp	Ala	Val	Ala	Glu	Ile	Asp
385					390				395						400
Ala	Leu	Tyr	Asp	Val	Tyr	Leu	Asp	Val	Gln	Glu	Lys	Trp	Gly	Leu	Glu
				405					410					415	

Asp Val Met Leu Met Gly Asp Phe Asn Ala Gly Cys Ser Tyr Val Arg
 420 425 430

Pro Ser Gln Trp Ser Ser Ile Arg Leu Trp Thr Ser Pro Thr Phe Gln
 435 440 445

Trp Leu Ile Pro Asp Ser Ala Asp Thr Thr Ala Thr Pro Thr His Cys
 450 455 460

Ala Tyr Asp Arg Ile Val Val Ala Gly Met Leu Leu Arg Gly Ala Val
 465 470 475 480

Val Pro Asp Ser Ala Leu Pro Phe Asn Phe Gln Ala Ala Tyr Gly Leu
 485 490 495

Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp His Tyr Pro Val Glu Val
 500 505 510

Met Leu Lys Gly Gly Gly Pro Lys Lys Lys Arg Lys Val
 515 520 525

<210> 86

<211> 1596

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 86

atgggatgga gctgtatcat cctcttcttg gtagcaacag ctacagggtgt ccactcccag	60
gtgcagctgg tgcagtctgg ggcagagggtg aaaaagcctg gggcctcagt gaagggtgtcc	120
tgcaaggctt ctggctacac cttcagtgcc tactggatag agtgggtgcg ccagggtcca	180
ggaaagggcc tcgagtgggt cggagagatt ttacctggaa gtaataattc tagatacaat	240
gagaagttca agggccgagt gacagtcact agagacacat ccacaaacac agcctacatg	300
gagctcagca gcctgaggtc tgaggacaca gccgtctatt actgtgcaag atcctacgac	360
tttgcttggt ttgcttactg gggccaaggg actctgggtca cagtctcctc agcctccacc	420
aagggcccat cggctcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg	480

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gccctgggct gcctgggtcaa ggactacttc cccgaaccgg tgacgggtgtc gtggaactca 540
ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac 600
tccctcagca gcgtgggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc 660
aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt 720
gacaaaactc acacatgctg tgtggagtgc ccaccgtgcc cagcacctga agggagcggc 780
gggctgaaga tcgcagcctt caacatccag acatttgggg agaccaagat gtccaatgcc 840
accctcgtca gctacattgt gcagatcctg agccgctacg acatcgccct ggtccaggag 900
gtcagagaca gccacctgac tgccgtgggg aagctgctgg acaacctcaa tcaggacgca 960
ccagacacct atcactacgt ggtcagtgag ccactgggac ggaacagcta taaggagcgc 1020
tacctgttcg tgtacaggcc tgaccagggtg tctgcgggtg acagctacta ctacgatgat 1080
ggctgcgagc cctgcgggaa cgacaccttc aaccgagagc cagccattgt caggttcttc 1140
tcccggttca cagaggtcag ggagtttgcc attgttcccc tgcattgcggc cccgggggac 1200
gcagtagccg agatcgacgc tctctatgac gtctacctgg atgtccaaga gaaatggggc 1260
ttggaggacg tcatgttgat gggcgacttc aatgcgggct gcagctatgt gagaccctcc 1320
cagtgggtcat ccatccgcct gtggacaagc cccaccttcc agtggctgat ccccgacagc 1380
gctgacacca cagctacacc cagcactgt gcctatgaca ggatcgtggg tgcagggatg 1440
ctgctccgag gggccgttgt tcccgactcg gctcttcctt ttaacttcca ggctgcctat 1500
ggcctgagtg accaactggc ccaagccatc agtgaccact atccagtgga ggtgatgctg 1560
aaggggggcg gacccaaaaa gaagcgcaag gtttga 1596

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<210> 87

<211> 1596

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 87

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atgggatgga gctgtatcat cctcttcttg gtagcaacag ctacagggtg ccactcccag 60
gtgcagctgg tgcagtctgg ggcagagggtg aaaaagcctg gggcctcagt gaagggtgtc 120
tgcaaggctt ctggctacac cttcagtgcc tactggatag agtgggtgcg ccagggtcca 180

```

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ggaaagggcc tcgagtgggt cggagagatt ttacctggaa gtaataattc tagatacaat 240
gagaagttca agggccgagt gacagtcact agagacacat ccacaaacac agcctacatg 300
gagctcagca gcctgaggtc tgaggacaca gccgtctatt actgtgcaag atcctacgac 360
tttgccctgggt ttgcttactg gggccaaggg actctgggtca cagtctcctc agcctccacc 420
aaggggcccat cgggtcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg 480
gccctggggt gcctgggtcaa ggactacttc cccgaaccgg tgacgggtgtc gtggaactca 540
ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac 600
tcctcagca gcgtgggtgac cgtgccctcc agcagcttgg gcaccagac ctacatctgc 660
aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt 720
gacaaaactc acacatgctg tgtcgagtgt ccaccgtgtc cagcaccaga ggggagcggc 780
gggctgaaga tcgcagcctt caacatccag acatttgggg agaccaagat gtccaatgcc 840
accctcgtca gctacattgt gcagatcctg agccgctacg acatcgccct ggtccaggag 900
gtcagagaca gccacctgac tgccgtgggg aagctgctgg acaacctcaa tcaggacgca 960
ccagacacct atcactacgt ggtcagtgag cactgggac ggaacagcta taaggagcgc 1020
tacctgttcg tgtacaggcc tgaccagggtg tctgcgggtg acagctacta ctacgatgat 1080
ggctgcgagc cctgcgggaa cgacaccttc aaccgagagc cagccattgt caggttcttc 1140
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gcagtagccg agatcgacgc tctctatgac gtctacctgg atgtccaaga gaaatggggc 1260
ttggaggacg tcatgttgat gggcgacttc aatgcgggct gcagctatgt gagaccctcc 1320
cagtgggtcat ccatccgcct gtggacaagc cccaccttcc agtggctgat ccccgacagc 1380
gctgacacca cagctacacc cacgcactgt gcctatgaca ggatcgtgggt tgcagggatg 1440
ctgctccgag gggccgttgt tcccgactcg gctcttccct ttaacttcca ggctgcctat 1500
ggcctgagtg accaactggc ccaagccatc agtgaccact atccagtgga ggtgatgctg 1560
aaggggggag gacccaaaaa gaagcgcaag gtttga 1596

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<210> 88

<211> 1605

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 88

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gccgccacca tgggatggag ctgtatcatc ctcttcttgg tagcaacagc tacaggtgtc      60
cactcccagg tgcagctggt gcagtctggg gcagaggtga aaaagcctgg ggcctcagtg      120
aaggtgtcct gcaaggcttc tggctacacc ttcagtgcct actggataga gtgggtgcgc      180
caggctccag gaaagggcct cgagtgggtc ggagagattt tacctggaag taataattct      240
agatacaatg agaagttcaa gggccgagtg acagtcacta gagacacatc cacaacaca      300
gcctacatgg agctcagcag cctgaggtct gaggacacag ccgtctatta ctgtgcaaga      360
tcctacgact ttgcctgggt tgcttactgg ggccaaggga ctctggtcac agtctcctca      420
gcctccacca agggcccatc ggtcttcccc ctggcacctt cctccaagag cacctctggg      480
ggcacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggt gacggtgtcg      540
tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca      600
ggactctact ccctcagcag cgtgggtgacc gtgccctcca gcagcttggg caccagacc      660
tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc      720
aatctttgtg acaaaaactca cacatgctgt gtcgagtgtc caccgtgtcc agcaccagag      780
gggagcggcg ggctgaagat cgcagccttc aacatccaga catttgggga gaccaagatg      840
tccaatgcca ccctcgtcag ctacattgtg cagatcctga gccgctacga catcgccctg      900
gtccaggagg tcagagacag ccacctgact gccgtgggga agctgctgga caacctcaat      960
caggacgcac cagacaccta tcactacgtg gtcagtgagc cactgggacg gaacagctat     1020
aaggagcgct acctgttcgt gtacaggcct gaccaggtgt ctgcggtgga cagctactac     1080
tacgatgatg gctgcgagcc ctgcgggaac gacaccttca accgagagcc agccattgtc     1140
aggttcttct cccggttcac agaggtcagg gagtttgcca ttgttccctt gcatgcggcc     1200
ccgggggacg cagtagccga gatcgacgct ctctatgacg tctacctgga tgtccaagag     1260
aatggggct tggaggacgt catgttgatg ggcgacttca atgcgggctg cagctatgtg     1320
agaccctccc agtggtcatc catccgcctg tggacaagcc ccaccttcca gtggctgatc     1380
cccgacagcg ctgacaccac agctacaccc acgcactgtg cctatgacag gatcgtgggtt     1440
gcaggggatgc tgctccgagg ggccgttggt cccgactcgg ctcttccctt taacttccag     1500
gctgcctatg gcctgagtga ccaactggcc caagccatca gtgaccacta tccagtggag     1560

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gtgatgctga aggggggcg acccaaaaag aagcgcaagg tttga

1605

<210> 89

<211> 1596

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<220>

<221> CDS

<222> (1)..(1596)

<223>

<400> 89

atg gga tgg agc tgt atc atc ctc ttc ttg gta gca aca gct aca ggt	48
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly	
1 5 10 15	

gtc cac tcc cag gtg cag ctg gtg cag tct ggg gca gag gtg aaa aag	96
Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys	
20 25 30	

cct ggg gcc tca gtg aag gtg tcc tgc aag gct tct ggc tac acc ttc	144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe	
35 40 45	

agt gcc tac tgg ata gag tgg gtg cgc cag gct cca gga aag ggc ctc	192
Ser Ala Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu	
50 55 60	

gag tgg gtc gga gag att tta cct gga agt aat aat tct aga tac aat	240
Glu Trp Val Gly Glu Ile Leu Pro Gly Ser Asn Asn Ser Arg Tyr Asn	
65 70 75 80	

gag aag ttc aag ggc cga gtg aca gtc act aga gac aca tcc aca aac	288
Glu Lys Phe Lys Gly Arg Val Thr Val Thr Arg Asp Thr Ser Thr Asn	
85 90 95	

aca gcc tac atg gag ctc agc agc ctg agg tct gag gac aca gcc gtc	336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val	
100 105 110	

tat tac tgt gca aga tcc tac gac ttt gcc tgg ttt gct tac tgg ggc	384
Tyr Tyr Cys Ala Arg Ser Tyr Asp Phe Ala Trp Phe Ala Tyr Trp Gly	
115 120 125	

caa	ggg	act	ctg	gtc	aca	gtc	tcc	tca	gcc	tcc	acc	aag	ggc	cca	tcg	432
Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	
130						135					140					
gtc	ttc	ccc	ctg	gca	ccc	tcc	tcc	aag	agc	acc	tct	ggg	ggc	aca	gcg	480
Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	
145					150					155					160	
gcc	ctg	ggc	tgc	ctg	gtc	aag	gac	tac	ttc	ccc	gaa	ccg	gtg	acg	gtg	528
Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	
				165					170					175		
tcg	tgg	aac	tca	ggc	gcc	ctg	acc	agc	ggc	gtg	cac	acc	ttc	ccg	gct	576
Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	
			180					185					190			
gtc	cta	cag	tcc	tca	gga	ctc	tac	tcc	ctc	agc	agc	gtg	gtg	acc	gtg	624
Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	
		195					200					205				
ccc	tcc	agc	agc	ttg	ggc	acc	cag	acc	tac	atc	tgc	aac	gtg	aat	cac	672
Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	
	210					215					220					
aag	ccc	agc	aac	acc	aag	gtg	gac	aag	aaa	gtt	gag	ccc	aaa	tct	tgt	720
Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	
225					230					235					240	
gac	aaa	act	cac	aca	tgc	tgt	gtg	gag	tgc	cca	ccg	tgc	cca	gca	cct	768
Asp	Lys	Thr	His	Thr	Cys	Cys	Val	Glu	Cys	Pro	Pro	Cys	Pro	Ala	Pro	
				245					250					255		
gaa	ggg	agc	ggc	ggg	ctg	aag	atc	gca	gcc	ttc	aac	atc	cag	aca	ttt	816
Glu	Gly	Ser	Gly	Gly	Leu	Lys	Ile	Ala	Ala	Phe	Asn	Ile	Gln	Thr	Phe	
			260					265					270			
ggg	gag	acc	aag	atg	tcc	aat	gcc	acc	ctc	gtc	agc	tac	att	gtg	cag	864
Gly	Glu	Thr	Lys	Met	Ser	Asn	Ala	Thr	Leu	Val	Ser	Tyr	Ile	Val	Gln	
		275					280					285				
atc	ctg	agc	cgc	tac	gac	atc	gcc	ctg	gtc	cag	gag	gtc	aga	gac	agc	912
Ile	Leu	Ser	Arg	Tyr	Asp	Ile	Ala	Leu	Val	Gln	Glu	Val	Arg	Asp	Ser	
	290					295					300					
cac	ctg	act	gcc	gtg	ggg	aag	ctg	ctg	gac	aac	ctc	aat	cag	gac	gca	960
His	Leu	Thr	Ala	Val	Gly	Lys	Leu	Leu	Asp	Asn	Leu	Asn	Gln	Asp	Ala	
305					310					315					320	
cca	gac	acc	tat	cac	tac	gtg	gtc	agt	gag	cca	ctg	gga	cgg	aac	agc	1008
Pro	Asp	Thr	Tyr	His	Tyr	Val	Val	Ser	Glu	Pro	Leu	Gly	Arg	Asn	Ser	
				325					330					335		
tat	aag	gag	cgc	tac	ctg	ttc	gtg	tac	agg	cct	gac	cag	gtg	tct	gcg	1056
Tyr	Lys	Glu	Arg	Tyr	Leu	Phe	Val	Tyr	Arg	Pro	Asp	Gln	Val	Ser	Ala	
			340				345						350			
gtg	gac	agc	tac	tac	tac	gat	gat	ggc	tgc	gag	ccc	tgc	ggg	aac	gac	1104
Val	Asp	Ser	Tyr	Tyr	Tyr	Asp	Asp	Gly	Cys	Glu	Pro	Cys	Gly	Asn	Asp	

355	360	365	
acc ttc aac cga gag cca gcc att gtc agg ttc ttc tcc cgg ttc aca Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe Thr 370 375 380			1152
gag gtc agg gag ttt gcc att gtt ccc ctg cat gcg gcc ccg ggg gac Glu Val Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly Asp 385 390 395 400			1200
gca gta gcc gag atc gac gct ctc tat gac gtc tac ctg gat gtc caa Ala Val Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val Gln 405 410 415			1248
gag aaa tgg ggc ttg gag gac gtc atg ttg atg ggc gac ttc aat gcg Glu Lys Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn Ala 420 425 430			1296
ggc tgc agc tat gtg aga ccc tcc cag tgg tca tcc atc cgc ctg tgg Gly Cys Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu Trp 435 440 445			1344
aca agc ccc acc ttc cag tgg ctg atc ccc gac agc gct gac acc aca Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr Thr 450 455 460			1392
gct aca ccc acg cac tgt gcc tat gac agg atc gtg gtt gca ggg atg Ala Thr Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly Met 465 470 475 480			1440
ctg ctc cga ggg gcc gtt gtt ccc gac tcg gct ctt ccc ttt aac ttc Leu Leu Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn Phe 485 490 495			1488
cag gct gcc tat ggc ctg agt gac caa ctg gcc caa gcc atc agt gac Gln Ala Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp 500 505 510			1536
cac tat cca gtg gag gtg atg ctg aag ggg ggc gga ccc aaa aag aag His Tyr Pro Val Glu Val Met Leu Lys Gly Gly Gly Pro Lys Lys Lys 515 520 525			1584
cgc aag gtt tga Arg Lys Val 530			1596

<210> 90

<211> 531

<212> PRT

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 90

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1 5 10 15

Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45

Ser Ala Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
50 55 60

Glu Trp Val Gly Glu Ile Leu Pro Gly Ser Asn Asn Ser Arg Tyr Asn
65 70 75 80

Glu Lys Phe Lys Gly Arg Val Thr Val Thr Arg Asp Thr Ser Thr Asn
85 90 95

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
100 105 110

Tyr Tyr Cys Ala Arg Ser Tyr Asp Phe Ala Trp Phe Ala Tyr Trp Gly
115 120 125

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
130 135 140

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145 150 155 160

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
165 170 175

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
180 185 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
195 200 205

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
210 215 220

Lys 225	Pro	Ser	Asn	Thr	Lys 230	Val	Asp	Lys	Lys	Val 235	Glu	Pro	Lys	Ser	Cys 240
Asp	Lys	Thr	His	Thr 245	Cys	Cys	Val	Glu	Cys 250	Pro	Pro	Cys	Pro	Ala 255	Pro
Glu	Gly	Ser	Gly 260	Gly	Leu	Lys	Ile	Ala 265	Ala	Phe	Asn	Ile	Gln 270	Thr	Phe
Gly	Glu	Thr 275	Lys	Met	Ser	Asn	Ala 280	Thr	Leu	Val	Ser	Tyr 285	Ile	Val	Gln
Ile 290	Leu	Ser	Arg	Tyr	Asp	Ile 295	Ala	Leu	Val	Gln	Glu 300	Val	Arg	Asp	Ser
His 305	Leu	Thr	Ala	Val	Gly 310	Lys	Leu	Leu	Asp	Asn 315	Leu	Asn	Gln	Asp	Ala 320
Pro	Asp	Thr	Tyr	His 325	Tyr	Val	Val	Ser	Glu 330	Pro	Leu	Gly	Arg	Asn 335	Ser
Tyr	Lys	Glu	Arg 340	Tyr	Leu	Phe	Val	Tyr 345	Arg	Pro	Asp	Gln	Val 350	Ser	Ala
Val	Asp	Ser 355	Tyr	Tyr	Tyr	Asp	Asp 360	Gly	Cys	Glu	Pro	Cys 365	Gly	Asn	Asp
Thr 370	Phe	Asn	Arg	Glu	Pro	Ala 375	Ile	Val	Arg	Phe	Phe 380	Ser	Arg	Phe	Thr
Glu 385	Val	Arg	Glu	Phe	Ala 390	Ile	Val	Pro	Leu	His 395	Ala	Ala	Pro	Gly	Asp 400
Ala	Val	Ala	Glu	Ile 405	Asp	Ala	Leu	Tyr	Asp 410	Val	Tyr	Leu	Asp	Val 415	Gln
Glu	Lys	Trp	Gly 420	Leu	Glu	Asp	Val	Met 425	Leu	Met	Gly	Asp	Phe 430	Asn	Ala
Gly	Cys	Ser 435	Tyr	Val	Arg	Pro	Ser 440	Gln	Trp	Ser	Ser	Ile 445	Arg	Leu	Trp
Thr 450	Ser	Pro	Thr	Phe	Gln	Trp 455	Leu	Ile	Pro	Asp	Ser 460	Ala	Asp	Thr	Thr

Ala Thr Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly Met
465 470 475 480

Leu Leu Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn Phe
485 490 495

Gln Ala Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp
500 505 510

His Tyr Pro Val Glu Val Met Leu Lys Gly Gly Gly Pro Lys Lys Lys
515 520 525

Arg Lys Val
530

<210> 91

<211> 1590

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 91

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tgcaaggctt ctggctacac cttcagtgcc tactggatag agtgggtgcg ccaggctcca	180
ggaaagggcc tcgagtgggt cggagagatt ttacctggaa gtaataattc tagatacaat	240
gagaagttca agggccgagt gacagtcact agagacacat ccacaaacac agcctacatg	300
gagctcagca gcctgaggtc tgaggacaca gccgtctatt actgtgcaag atcctacgac	360
tttgccctggg ttgcttactg gggccaaggg actctgggtca cagtctcctc agcctccacc	420
aaggggcccat cggctcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg	480
gccctggggt gcctgggtcaa ggactacttc cccgaaccgg tgacgggtgtc gtggaactca	540
ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac	600
tcctcagca gcgtgggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc	660

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aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt 720
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aagatcgcag ccttcaacat ccagacattt ggggagacca agatgtccaa tgccaccctc 840
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gacagccacc tgactgccgt ggggaagctg ctggacaacc tcaatcagga cgcaccagac 960
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gccgagatcg acgtctctta tgacgtctac ctggatgtcc aagagaaatg gggcttggag 1260
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accacagcta caccacgca ctgtgcctat gacaggatcg tggttgcagg gatgctgctc 1440
cgagggggccg ttgttcccga ctcggtcttt ccctttaact tccaggctgc ctatggcctg 1500
agtgaccaac tggccaagc catcagtgac cactatccag tggaggtgat gctgaagggg 1560
ggcggaccca aaaagaagcg caaggtttga 1590

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<210> 92

<211> 1590

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 92

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gtgcagctgg tgcagtctgg ggcagagggtg aaaaagcctg gggcctcagt gaagggtgtcc 120
tgcaaggctt ctggctacac cttcagtgcc tactggatag agtgggtgcg ccagggtcca 180
ggaaagggcc tcgagtgggt cggagagatt ttacctggaa gtaataattc tagatacaat 240
gagaagttca agggccgagt gacagtcact agagacacat ccacaaacac agcctacatg 300
gagctcagca gcctgagggtc tgaggacaca gccgtctatt actgtgcaag atcctacgac 360

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tttgccctggt ttgcttactg gggccaaggg actctgggtca cagtctcctc agcctccacc 420
aagggcccat cggtcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg 480
gccctggggt gcctgggtcaa ggactacttc cccgaaccgg tgacgggtgtc gtggaactca 540
ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcttc aggactctac 600
tcctcagca gcgtgggtgac cgtgccctcc agcagcttgg gcaccagac ctacatctgc 660
aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt 720
gacaaaactc acacatgctg tgtcgagtgt ccaccgtgtc cagcaccaga gggcgggctg 780
aagatcgag ccttcaacat ccagacattt ggggagacca agatgtccaa tgccaccctc 840
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gacagccacc tgactgccgt ggggaagctg ctggacaacc tcaatcagga cgcaccagac 960
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gccgagatcg acgtctctta tgacgtctac ctggatgtcc aagagaaatg gggcttgag 1260
gacgtcatgt tgatgggcga cttcaatgcg ggctgcagct atgtgagacc ctcccagtgg 1320
tcatccatcc gcctgtggac aagccccacc ttccagtggc tgatccccga cagcgctgac 1380
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cgagggggcg ttgttcccga ctcggtcttt ccctttaact tccaggctgc ctatggcctg 1500
agtgaccaac tggccaagc catcagtgc cactatccag tggaggtgat gctgaagggg 1560
ggcggacca aaaagaagcg caaggtttga 1590

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<210> 93

<211> 1599

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 93

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gccgccacca tgggatggag ctgtatcatc ctcttcttgg tagcaacagc tacagggtgtc      60
cactcccagg tgcagctggg gcagtctggg gcagaggtga aaaagcctgg ggcctcagtg      120
aagggtgtcct gcaaggcttc tggctacacc ttcagtgcct actggataga gtgggtgcgc      180
caggctccag gaaagggcct cgagtgggtc ggagagattt tacctggaag taataattct      240
agatacaatg agaagttcaa gggccgagtg acagtcacta gagacacatc cacaacaca      300
gcctacatgg agctcagcag cctgaggtct gaggacacag ccgtctatta ctgtgcaaga      360
tcctacgact ttgcctgggt tgcttactgg ggccaaggga ctctgggtcac agtctcctca      420
gcctccacca agggcccatc ggtcttcccc ctggcacctt cctccaagag cacctctggg      480
ggcacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggt gacgggtgtcg      540
tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca      600
ggactctact ccctcagcag cgtgggtgacc gtgccctcca gcagcttggg caccagacc      660
tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc      720
aaatcttgtg acaaaaactca cacatgctgt gtcgagtgtc caccgtgtcc agcaccagag      780
ggcgggctga agatcgcagc cttcaacatc cagacatttg gggagaccaa gatgtccaat      840
gccaccctcg tcagctacat tgtgcagatc ctgagccgct acgacatcgc cctgggtccag      900
gaggtcagag acagccacct gactgccgtg gggaaagtgc tggacaacct caatcaggac      960
gcaccagaca cctatcacta cgtgggtcagt gagccactgg gacggaacag ctataaggag     1020
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gatggctgcg agccctgcgg gaacgacacc ttcaaccgag agccagccat tgtcagggttc     1140
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tcccagtggt catccatccg cctgtggaca agccccacct tccagtgggt gatccccgac     1380
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tatggcctga gtgaccaact ggccaagcc atcagtgacc actatccagt ggaggatgat     1560
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<210> 94

<211> 1590

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<220>

<221> CDS

<222> (1)..(1590)

<223>

<400> 94

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Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly	
1 5 10 15	

gtc cac tcc cag gtg cag ctg gtg cag tct ggg gca gag gtg aaa aag	96
Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys	
20 25 30	

cct ggg gcc tca gtg aag gtg tcc tgc aag gct tct ggc tac acc ttc	144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe	
35 40 45	

agt gcc tac tgg ata gag tgg gtg cgc cag gct cca gga aag ggc ctc	192
Ser Ala Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu	
50 55 60	

gag tgg gtc gga gag att tta cct gga agt aat aat tct aga tac aat	240
Glu Trp Val Gly Glu Ile Leu Pro Gly Ser Asn Asn Ser Arg Tyr Asn	
65 70 75 80	

gag aag ttc aag ggc cga gtg aca gtc act aga gac aca tcc aca aac	288
Glu Lys Phe Lys Gly Arg Val Thr Val Thr Arg Asp Thr Ser Thr Asn	
85 90 95	

aca gcc tac atg gag ctc agc agc ctg agg tct gag gac aca gcc gtc	336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val	
100 105 110	

tat tac tgt gca aga tcc tac gac ttt gcc tgg ttt gct tac tgg ggc	384
Tyr Tyr Cys Ala Arg Ser Tyr Asp Phe Ala Trp Phe Ala Tyr Trp Gly	
115 120 125	

caa ggg act ctg gtc aca gtc tcc tca gcc tcc acc aag ggc cca tcg	432
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser	
130 135 140	

gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg	480
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala	

145					150					155					160	
gcc	ctg	ggc	tgc	ctg	gtc	aag	gac	tac	ttc	ccc	gaa	ccg	gtg	acg	gtg	528
Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	
				165					170					175		
tcg	tgg	aac	tca	ggc	gcc	ctg	acc	agc	ggc	gtg	cac	acc	ttc	ccg	gct	576
Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	
			180					185					190			
gtc	cta	cag	tcc	tca	gga	ctc	tac	tcc	ctc	agc	agc	gtg	gtg	acc	gtg	624
Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	
		195					200					205				
ccc	tcc	agc	agc	ttg	ggc	acc	cag	acc	tac	atc	tgc	aac	gtg	aat	cac	672
Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	
	210					215					220					
aag	ccc	agc	aac	acc	aag	gtg	gac	aag	aaa	gtt	gag	ccc	aaa	tct	tgt	720
Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	
225					230				235						240	
gac	aaa	act	cac	aca	tgc	tgt	gtg	gag	tgc	cca	ccg	tgc	cca	gca	cct	768
Asp	Lys	Thr	His	Thr	Cys	Cys	Val	Glu	Cys	Pro	Pro	Cys	Pro	Ala	Pro	
				245				250						255		
gaa	ggc	ggg	ctg	aag	atc	gca	gcc	ttc	aac	atc	cag	aca	ttt	ggg	gag	816
Glu	Gly	Gly	Leu	Lys	Ile	Ala	Ala	Phe	Asn	Ile	Gln	Thr	Phe	Gly	Glu	
			260					265					270			
acc	aag	atg	tcc	aat	gcc	acc	ctc	gtc	agc	tac	att	gtg	cag	atc	ctg	864
Thr	Lys	Met	Ser	Asn	Ala	Thr	Leu	Val	Ser	Tyr	Ile	Val	Gln	Ile	Leu	
		275					280					285				
agc	cgc	tac	gac	atc	gcc	ctg	gtc	cag	gag	gtc	aga	gac	agc	cac	ctg	912
Ser	Arg	Tyr	Asp	Ile	Ala	Leu	Val	Gln	Glu	Val	Arg	Asp	Ser	His	Leu	
	290					295					300					
act	gcc	gtg	ggg	aag	ctg	ctg	gac	aac	ctc	aat	cag	gac	gca	cca	gac	960
Thr	Ala	Val	Gly	Lys	Leu	Leu	Asp	Asn	Leu	Asn	Gln	Asp	Ala	Pro	Asp	
305					310				315						320	
acc	tat	cac	tac	gtg	gtc	agt	gag	cca	ctg	gga	cgg	aac	agc	tat	aag	1008
Thr	Tyr	His	Tyr	Val	Val	Ser	Glu	Pro	Leu	Gly	Arg	Asn	Ser	Tyr	Lys	
				325					330					335		
gag	cgc	tac	ctg	ttc	gtg	tac	agg	cct	gac	cag	gtg	tct	gcg	gtg	gac	1056
Glu	Arg	Tyr	Leu	Phe	Val	Tyr	Arg	Pro	Asp	Gln	Val	Ser	Ala	Val	Asp	
			340					345					350			
agc	tac	tac	tac	gat	gat	ggc	tgc	gag	ccc	tgc	ggg	aac	gac	acc	ttc	1104
Ser	Tyr	Tyr	Tyr	Asp	Asp	Gly	Cys	Glu	Pro	Cys	Gly	Asn	Asp	Thr	Phe	
		355					360					365				
aac	cga	gag	cca	gcc	att	gtc	agg	ttc	ttc	tcc	cgg	ttc	aca	gag	gtc	1152
Asn	Arg	Glu	Pro	Ala	Ile	Val	Arg	Phe	Phe	Ser	Arg	Phe	Thr	Glu	Val	
	370					375					380					
agg	gag	ttt	gcc	att	gtt	ccc	ctg	cat	gcg	gcc	ccg	ggg	gac	gca	gta	1200

Arg	Glu	Phe	Ala	Ile	Val	Pro	Leu	His	Ala	Ala	Pro	Gly	Asp	Ala	Val		
385					390				395						400		
gcc	gag	atc	gac	gct	ctc	tat	gac	gtc	tac	ctg	gat	gtc	caa	gag	aaa	1248	
Ala	Glu	Ile	Asp	Ala	Leu	Tyr	Asp	Val	Tyr	Leu	Asp	Val	Gln	Glu	Lys		
				405				410					415				
tgg	ggc	ttg	gag	gac	gtc	atg	ttg	atg	ggc	gac	ttc	aat	gcg	ggc	tgc	1296	
Trp	Gly	Leu	Glu	Asp	Val	Met	Leu	Met	Gly	Asp	Phe	Asn	Ala	Gly	Cys		
			420				425					430					
agc	tat	gtg	aga	ccc	tcc	cag	tgg	tca	tcc	atc	cgc	ctg	tgg	aca	agc	1344	
Ser	Tyr	Val	Arg	Pro	Ser	Gln	Trp	Ser	Ser	Ile	Arg	Leu	Trp	Thr	Ser		
		435				440					445						
ccc	acc	ttc	cag	tgg	ctg	atc	ccc	gac	agc	gct	gac	acc	aca	gct	aca	1392	
Pro	Thr	Phe	Gln	Trp	Leu	Ile	Pro	Asp	Ser	Ala	Asp	Thr	Thr	Ala	Thr		
	450					455				460							
ccc	acg	cac	tgt	gcc	tat	gac	agg	atc	gtg	gtt	gca	ggg	atg	ctg	ctc	1440	
Pro	Thr	His	Cys	Ala	Tyr	Asp	Arg	Ile	Val	Val	Ala	Gly	Met	Leu	Leu		
465				470				475						480			
cga	ggg	gcc	gtt	gtt	ccc	gac	tcg	gct	ctt	ccc	ttt	aac	ttc	cag	gct	1488	
Arg	Gly	Ala	Val	Val	Pro	Asp	Ser	Ala	Leu	Pro	Phe	Asn	Phe	Gln	Ala		
			485				490						495				
gcc	tat	ggc	ctg	agt	gac	caa	ctg	gcc	caa	gcc	atc	agt	gac	cac	tat	1536	
Ala	Tyr	Gly	Leu	Ser	Asp	Gln	Leu	Ala	Gln	Ala	Ile	Ser	Asp	His	Tyr		
		500					505					510					
cca	gtg	gag	gtg	atg	ctg	aag	ggg	ggc	gga	ccc	aaa	aag	aag	cgc	aag	1584	
Pro	Val	Glu	Val	Met	Leu	Lys	Gly	Gly	Gly	Pro	Lys	Lys	Lys	Arg	Lys		
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gtt	tga															1590	
Val																	

<210> 95

<211> 529

<212> PRT

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 95

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			20					25					30					
Pro	Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe			
		35					40					45						
Ser	Ala	Tyr	Trp	Ile	Glu	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu			
	50					55					60							
Glu	Trp	Val	Gly	Glu	Ile	Leu	Pro	Gly	Ser	Asn	Asn	Ser	Arg	Tyr	Asn			
65					70					75					80			
Glu	Lys	Phe	Lys	Gly	Arg	Val	Thr	Val	Thr	Arg	Asp	Thr	Ser	Thr	Asn			
				85					90					95				
Thr	Ala	Tyr	Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val			
			100					105					110					
Tyr	Tyr	Cys	Ala	Arg	Ser	Tyr	Asp	Phe	Ala	Trp	Phe	Ala	Tyr	Trp	Gly			
		115					120					125						
Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser			
	130					135					140							
Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala			
145					150					155					160			
Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val			
				165					170					175				
Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala			
			180					185					190					
Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val			
		195					200					205						
Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His			
	210					215					220							
Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys			
225					230					235					240			
Asp	Lys	Thr	His	Thr	Cys	Cys	Val	Glu	Cys	Pro	Pro	Cys	Pro	Ala	Pro			
				245					250					255				

Glu Gly Gly Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr Phe Gly Glu
 260 265 270

Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val Gln Ile Leu
 275 280 285

Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp Ser His Leu
 290 295 300

Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp Ala Pro Asp
 305 310 315 320

Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn Ser Tyr Lys
 325 330 335

Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser Ala Val Asp
 340 345 350

Ser Tyr Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn Asp Thr Phe
 355 360 365

Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe Thr Glu Val
 370 375 380

Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly Asp Ala Val
 385 390 395 400

Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val Gln Glu Lys
 405 410 415

Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn Ala Gly Cys
 420 425 430

Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu Trp Thr Ser
 435 440 445

Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr Thr Ala Thr
 450 455 460

Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly Met Leu Leu
 465 470 475 480

Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn Phe Gln Ala

148

485

490

495

Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp His Tyr
500 505 510

Pro Val Glu Val Met Leu Lys Gly Gly Gly Pro Lys Lys Lys Arg Lys
515 520 525

Val

<210> 96

<211> 7

<212> PRT

<213> Simian virus 40

<400> 96

Pro Lys Lys Lys Arg Lys Val
1 5

<210> 97

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Polypeptide linker

<400> 97

Gly Ser Gly Gly
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<210> 98

<211> 9

<212> DNA

<213> Artificial Sequence

<220>

<223> Consensus ribosome binding sequence

<400> 98
gccgccacc

9

<210> 99

<211> 35

<212> PRT

<213> Artificial Sequence

<220>

<223> Fusion protein

<400> 99

Pro Asp Thr Arg Pro Pro Asp Thr Arg Pro Pro Asp Thr Arg Pro Pro
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Asp Thr Arg Pro Pro Asp Thr Arg Pro Pro Asp Thr Arg Pro Pro Asp
20 25 30

Thr Arg Pro
35

<210> 100

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant hinge

<400> 100

Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Glu
1 5 10

<210> 101

<211> 5

<212> PRT

<213> Homo sapiens

<400> 101

Ala Pro Asp Thr Arg
1 5

A35-
cut